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J. Biol. Chem. 27275995_6003(1997)... -i- FUNCTION: COMPONENT OF THE CIRCADIAN CLOCK OR DOWNSTREAM EFFECTOR OF CLOCK FUNCTION. EXHIBITS A HIGH AMPLITUDE CIRCADIAN RHYTHM MITH MAXIMAL LEVELS IN EARLY EVENING. IN CONSTANT DARKNESS OR CONSTANT LIGHT, THE AMPLITUDE OF THE RHYTHM DECREASES (BY SIMILARITY). -i- SIMILARITY: BELONGS TO THE CCR4/NOCTURIN FAMILY. EMBL; AF183960; AAD56547.1; -. EMBL; AF199491; AAG01384.1; -. EMBL; U70139; AAB62717.1; ALT_! use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way Wang Y., Osterbur D.L., Green C.B., Besharse J.C., "Mammalian homologs of Xenopus nocturnin: conserva and circadian regulation."; STRAIN-BALB/C; TISSUE-Brain; MEDLINE-99453012; PubMed-10521507; Dupressoir A., Barbot W., Loireau M.P., Heidmann T.; "Characterization of a mammalian gene related to the yeast CCR4 general transcription factor and revealed by transposon insertion."; J. Biol. Chem. 274:31068-31075(1999). Puech A., Dupressoir A., Loireau M.P., Mattei M.-G., Heidmann T.; "Characterization of two age induced intractisternal A-particle-related transcripts in the mouse liver. Transcriptional read-through into an open reading frame-with-similarities to the yeast ccr4 transcription STRAIN=DBA/2J; TISSUE=Liver; MEDLINE=97190339; PubMed=9038221; 035710; Q9QZG9; 15-JUL-1999 (Rel. 38, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Nocturnin (CCR4 protein homolog). SEQUENCE OF 62-429 FROM N.A. Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases SEQUENCE FROM N.A. STRAIN=BALB/C; TISSUE=Retina; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus SEQUENCE FROM N.A. NCBI_TaxID=10090; Mus musculus (Mouse) (See http://www.isb-sib.ch/announce/ conservation of structure Usage уд and for

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SEQUENCE
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Proc. Natl. Acad. Sci. U.S.A. 93:14884-14888(1996).

Proc. Natl. Acad. Sci. U.S.A. 93:14884-14888 (1996).

Proc. Natl. Acad. Sci. U.S.A. 93:14884-1488 (1996).

Proc. Natl. Acad. Sci. U.S.A. 93:14884 (1996
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                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Retinal photoreceptors; MEDLINE-97121484; PubMed-8962150;
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15-JUN-2002 (Rel. 41, Last annotation update)
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE-99453012; PubMed-10521507; Dupressoir A., Barbot W., Loireau M.P., Heidmann T.; Dupressoir A., Barbot W., Loireau M.P., Heidmann T.; "Characterization of a mammalian gene related to the yeast CCR4 general transcription factor and revealed by transposon insertigeneral factor and revealed by transposon insertigeneral factor and revealed by transposon factor and revealed by t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOCT_HUMAN STANDARD; PRT; 431 AA.
Q9UK39; Q9HD93; Q9HD94; Q9HD95;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nocturnin (CCR4 protein homolog).
CCRN4L OR NOC OR CCR4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
        and circadian regulation.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COMPONENT OF THE CIRCADIAN CLOCK OR DOWNSTREAM EFFECTOR OF CLOCK FUNCTION. EXHIBITS A HIGH AMPLITUDE CIRCADIAN RHYTHM WITH MAXIMAL LEYELS IN EARLY EVENING. IN CONSTANT DARKNESS OR CONSTANT LIGHT, THE AMPLITUDE OF THE RHYTHM DECREASES (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CCR4/NOCTURIN FAMILY.
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Pfam; PF03372; Exo_endo_phos; 1.
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Eukaryota; Metazoa;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                            Wanng Y., Osterbur D.L., Green C.B., Beshau
Mammalian homologs of Xenopus nocturnin:
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388 AA;
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CONFLICT
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EMBL; AF199492; AAG01387.1; -.
EMBL; AF199493; AAG01388 1; -.
EMBL; AF199494; AAG01389.1; -.
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
NCBI_TaxID=44689;
                                                                     01-oCT-1996 (Rel. 34, Created)
01-oCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA-(apurinic or apyrimidinic site) lyase (EC
                                                                                                                               APEA_DICDI
P51173;
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                             Dictyostelium discoideum (Slime mold).
                                                        apurinic/apyrimidinic(AP)-endonuclease).
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                                                                                                                                                                                                                                                                                                          MNSNLGITAACKLRFDRIFFRAAAEEGHIIPRSLDLL-----GLEKLDCGRFPSDHWGLL
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                                                                                                                                                                                                                                                                            ---KIRTSGECRHTLDYIWYSKHALN---VRSALDLLTEEQIGPNRLPSFNYPSDHLSLV 418
                                                                                                                                                                                                                                                                                                                                                                   MQEAPESATY -- IFAGDTNLR-DREVTRCGGLPN-NIVDVWEFL---GKPKHCQYTWDTQ
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431 AA;
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                                                                                                                                             STANDARD;
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Pred. No. 0.0057;
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-> A (IN REF. 2).
-> T (IN REF. 2; AAG01389).
-> S (IN REF. 2).
B61EF484E8D29AF5 CRC64;
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                                                                        4.2.99.18) (Class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 431;
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SEQUENCE FROM N.A.
MEDLINE-96226184; PubMed-8657579;
Freeland T.M., Guyer R.B., Ling A.Z., Deering R.A.;
"Apurinic/apyrimidinic (AP) endonuclease from Dictyostelium
"Apurinic/apyrimidinic nucleotide sequence and induction by su
                                                                                                                                                                                                                                                                                                                                                     METAL
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF03372; Exo_endo_phos; 1.
TIGRFAMS; TIGR00195; exoDNase_III; 1.
TIGRFAMS; TIGR00633; xth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DictyDb; DD05067; apeA.
InterPro; IPR000097; APendonclse1.
InterPro; IPR004442; ExoDNase_III.
InterPro; IPR004808; Exo_III_xth.
InterPro; IPR005135; Exo_endo_phos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U31631; AAC47024.1; -. HSSP; P27695; 1HD7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                DNA repair; Lyase; Nuclear DOMAIN 27 39 DOMAIN 41 44 DOMAIN 70 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNNG, GAMMA RAYS, BLEOMYCIN, AND STREPTOZOTOCIN.
-1- SIMILARITY: BELONGS TO THE AP/EXOA FAMILY OF DNA REPAIR ENZYMES.
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                                                                                                                                                                                                                                            EGGREAAEEEGEPEVKKRRLLCVEFASVASCDAAVAQCFLAENDWEMERALNSYFEPPVE
                            TRGHAAERMNQLKMVLKK------MQEAPESATVIFAGDTNLRDREV
                                                                                                                                       DLNNLSERARGYCSYLALYSPDYIFLQEV-IPPYYSYLKK----RSSNYEIITGHEEGYF
                                                                                                                                                                   KAAAKKKSK--DEDEDEEEKEEEEETNKTTASVSIAIDNLDEPKVEENQMKIISWNVAGF
                                                                                                                                                                                               ESALERRPETISEPKTYVDLTNEETTDSTTSKISPSEDTQQE----NGSMFSLITWNIDGL 124
                                                       GTGVLTKKK---
                                                                                 -TAIMLKKSRVKLKSQEIIPFPSTKMMRNLLCVHVNVSGNELCL-----MTSHLES--
                                                                                                                                                                                                                          EEEKEEVEEE-EEEDKKRKLVKKTPAKKA----
   TRG----
                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                             -SVLSKGFTECVEKENPDVLCLQETKINP--SNIKKDQMPKGYEYHFIEADQKGHH
                                                                                                                                                                                                                                                                                                                                       361 AA;
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351
--LQRLDYRIKEWDVDFQAYLEKLNATKPIIWCGDLNVAHTEI
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                                                       PNAITEGIGIAKHDN-EGRVITLEYVQFYIVNTYIPNAG
                                                                                                                                                                                                                                                                                 52;
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                                                                                                                                                                                                                                                                                Score 110.5;
Pred. No. 0.12
52; Mismatches
                                                                                                                                                                                                                                                                                                                                                    NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
POLY-GLU.
MAGRESIUM OR MANGANESE (BY SIMILARITY).
GENERAL BASE (BY SIMILARITY).
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Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Cherry Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Inositol phosphosphingolipids phospholipase C
phospholipase C) (IPS-PLC) (Neutral sphingomye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISC1_YEAST P40015;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of ISC1 (YER019w) as inositol phospholipase C in Saccharomyces cerevisiae."; J. Biol. Chem. 275:39793-39798(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales;
NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                     entities re
or send an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION. MEDLINE=20564359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (nSMase)
                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                               RANSMEM
                                                                                                                                                                                                                                                                                                                             [nterPro;
                                 146
                                                              13
                                                                                              90
   73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Responsible for the hydrolysis of the phosphosphingolipids (IPS), inositol phosphosylceramide (MIPC), and mannosyldiir phosphorylceramide (MICP), and mannosyldiir phosphorylceramide (M(IP)2C). Also active on sphingomyelin, this activity is probably not physiologically relevant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE NEUTRAL SPHINGOMYELINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COFACTOR: Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way field and this statement is not removed. Usage by and for commercial field and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                          50000821;
LTPISDELLPNGGDSNENEDYDVIALQEIWCVEDWKYLASACASKYPYQRLFHSGILTGP
                                                               KEDGQSEFEALNGTNAIMSDNSKAYSIKFLTFNTWGLKYVSKHRKERLRAIADKLAGHSM
                                                                                          EETTDSTTSKISPSEDTQQENGSMFSL--ITWNIDGLDL--NNLSERARGVCSYLALYSP 145
                                                                                                                                                                                                                                                                                                                                                          U18778; AAB64552.1;
                                                                                                                                                                                                                                                                                                            PF03372; Exo_endo_phos
PF03372; Exo_endo_phos; 1.
                                                                                                                          Similarity 22.0
78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                 Okamoto
                                                                                                                                                                                 334
477
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                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     svisiae (Baker's yeast).
Ascomycota; Saccharomycotina; Saccharomyces; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=11006294;
Y., Luberto C.,
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53940
                                                                                                                                          5.7%;
22.0%;
                                                                                                                                                                                         W.
                                   DVIFLQEV-IPPYYSYLKKR-SSNYEIITGHEEGYFT--
                                                                                                                            47;
                                                                                                                                                                                     MAGNESIUM (BY SIMILARITY).
IMPORTANT FOR SUBSTRATE RECOG
SIMILARITY).
GENERAL BASE (BY SIMILARITY).
; 0670FD303FEB8EFF CRC64;
                                                                                                                                          Score 108;
Pred. No. 0
                                                                                                                              Mismatches
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                                                                                                                                                         BG
                                                                                                                                            . 28;
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                                                                                                                                                         Length
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                                                                                                                              Indels
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mannosyldiinositol
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Cherry J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domae
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15-JUL-1998
16-OCT-2001
                                                                                                                                                                                                                                                          Yano M., Horiuchi T.; "A 718-kb DNA sequence of the Escherichia corresponding to the 12.7-28.0 min region DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                           MEDIJINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Aiba H., Baba T., Fujita K., Kanai K., Kashimoto K.
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Misobuchi Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Misobuchi Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blattner F.R., Plunkett G. III, Bloch C.A., Perr
Riley M., Collado-Vides J., Glasner J.D., Rode (
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YBHP_ECOLI P75772;
                                                                                                   Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbock E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli, and Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein ybhP.
YBHP OR B0790 OR Z1009 OR
STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M.,
Han C.-G., Ohtsubo E., Nakayama K.
                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-K
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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"The complete genome sequence Science 277:1453-1474(1997).
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                                                             SEQUENCE
                                                                                                                                                                                                           MEDLINE=21074935; PubMed=11206551;
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(Rel. 36, Last sequence up
(Rel. 40, Last annotation
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   Ohnishi M.,
Nakayama K.,
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                   Kurokawa K.,
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      Murata
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      Tanaka
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                   Ishii
                                                                                                                                                                                                                                                                                                     genome
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Mayhew G.F.,
       ≅ ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rose
                                                                                                                                                                                                                                                                                      map.";
       Yokoyama
Tobe T.,
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                                                                                                                                                                                                                                                                                                                                                Saito
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                  MEDLINE-99087487; PubMed-9872452;
Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XI.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
                                                                                                                                                                                                                                   O9UNK9: O94859;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein KIAAO759.
                                                                                                                                                                           Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                    TISSUE=Brain;
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                              NCBI_TaxID=9606
                                                                                                                                                                                                                          KIAA0759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 8:11-22(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLKMVLKKMQEAPESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWDT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVSVDGAEKRGVLYCRIVP-PMTGKAIHVMCVHLGL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHEVHPLHVENWPDTSHYEFLADTMWSDFAYGRNAVYPEGHHGNAVL--SRYPIEHYENR 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---IPPYYSYLKKRSSNYEIITG-------HEEGYFTAIMLKKSRVKLKSQE-- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DQTQQFS---FKVLTINIHKGFTAFNRRFILPELRDAVRTV-----SADIVCLQEVMG
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PF03372; Exo_endo_phos; 1.
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Tence4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
           5:277-286(1998).
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                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                           Chordata;
Primates;
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Pred. No. 0.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -REAHRQA 152
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RESULT 8
G6PL_YERPE
ID G6PL_Y
AC Q8ZAS2
DT 15-JUN
DT 15-
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Best Local
                                                                                                                                   Q8ZASZ;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glucose-6-phosphate isomerase (EC 5.3.1.9) (G
                                                                                                              isomerase) (PGI) (Phosphohexose
PGI OR YPO3718.
                                                                                                                                                                                                                                                                                                               G6PI_YERPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                           Bacteria; Proteobacteria;
                                                                                   Yersinia pestis
NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF03372; Exo_endo_phos; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB018302; BAA34479.1; ALT_INIT. EMBL; AL137268; CAB70667.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF111169; AAD44362.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nitted (JUL-1999) to the EMBL/GenBank/DDBJ databases SIMILARITY: BELONGS TO THE CCR4/NOCTURIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYQRKLQAPLWPSSLGITDCCQ 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARLSDGSHCPIILCGDLNSVPDSPLYNFIRDGEL-QYHGMP-----AWKVSGQEDFSHQ 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGSMWAAIPMQSEPQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TWDTQMN----SNLGITAACK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KMMRN------LLCVHV-----NVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLMSYNILAQDLMQQSSELYLHCHPDILNWNYRFVNLMQEFQHWDPDILCLQEVQEDHYW
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670 AA; 75275 MW;
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                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----NLSERARGVCSYLALYSPDVIFLQEVIPPYY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -TGCKTDG---CAVCYKPTRFRLLCASPVEYFRPGL
                                                        subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3D40E26813E27D83 CRC64;
                                                                                                                                   3C 5.3.1.9) (GPI) isomerase) (PHI).
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                                                                                                                                                                (Phosphoglucose
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RESULT 9
EX3_HAEIN
ID EX3_H
AC P4431
DT 01-NC
DT 01-NC
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 EX3_HAEIN
P44318;
01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0662; G6PISOMERASE.

PROSTTE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.

PROSTTE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.

Isomerase; Gluconeogenesis; Glycolysis; Complete ACT_SITE 386 BY SIMILARITY.

ACT_SITE 514 514 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CO-92 / Biovar Orientalis;

MEDLINB-21470413; PubMed-11586360;

Parkhill J. Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinla pestis, the causative agent of plague.";

Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001672; G6P_Isomerase
Pfam; PF00342; PGI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                        149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATHWAY: Involved in glycolysis and in gluconeogenesis SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: BELONGS TO THE GPI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose
                                                                                                                                              W----
                                                                                                                                                                            WDTQMNSNLGITAACKLRF-------DRIFFRAAAEEGHIIPRSLDLLGL
                                                                                                                                                                                                               HSARDWFLSAAGDPAHVAKHFAALSTNA--KAVGEFGIDTNNMFEFWDWVGG
                                                                                                                                                                                                                                                                                                                    -- NLLCVHVNVSGNELCLMTSHLESTRGHAAERMNQLK-----MVLKKMQEAPESAT--
                                                                                                                                                                                                                                                                                                                                                      DGKDVMPEVNAVLAKMKQFCDRVISGDWKGYTGKAITDVVNIGIGGSDLGPYMVTEALRP
                                                                                                                                                                                                                                                                                                                                                                        FLQEVIPPYYSYLKKRSSNYE-IITGHEEGYFTAIMLKKSRVKLKSQEIIPFPSTKMMR-::|:| : |: |: |: |: |: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                         KISPSEDTQQENG-----SMFSLITWNIDGLDLNNLSERARGVCSYLAL----YSPDVI 148
                                                                                                                                                                                                                                                                                                                                                                                                                       KL---QDLAKETDLAGAIKSMFS-----GEKINRTEDRA---VLHIALRNRSNTPIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                            -SAIGLSIALSVGFEHFEQLLSGAHAMDKHFAETPAEKN--LPVLLALIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    548 AA;
     (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                         STANDARD;
                                                                                                                                                                                                                                                                                 -----FVSNVDGT--HIAEALKPLNPETTLFLVASKTFTTQETMTNA
32, Created)32, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  514 I
61161 MW;
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21.1%;
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                                                                                                                                                                                                                                               ----TNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 103;
Pred. No. (
                                                       PRT;
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                                                                                                                          Qy
                                                                                                                                                                                                                              Query Match
Best Local S
Matches 59
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STRAIN-Rd / KW20 / ATCC 51907;

MEDLINE-95350630; PubMed-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Witerback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000097; APendonclsel.
InterPro; IPR004442; ExcDNase_III.
InterPro; IPR004808; ExcIII_xth.
InterPro; IPR005135; Exc_endo_phos.
Pfam; PF03372; Exc_endo_phos; 1.
TIGRRAMS; TIGR00195; excDNase_III; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U32689; AAC21719.1; HSSP; P09030; 1AKO. TIGR; H10041; --
                                                                                                                                                                                                                                                                                       PROSITE; PS00726; AP_NUCLEASE_F1_1; 1.
PROSITE; PS00727; AP_NUCLEASE_F1_2; 1.
PROSITE; PS00728; AP_NUCLEASE_F1_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Last Exodeoxyribonuclease III (F XTHA OR HI0041.
                                                                                                                                                                                                                           Hydrolase; Nuclease; Exonuclease; DNA repair; Complete proteome.

METAL

MAGNESIUM OR MANGANESE (BY SIMILARITY).

ACT_SITE 259 259 GENERAL BASE (BY SIMILARITY).

SEQUENCE 267 AA; 31025 MW; 6B3ADE465AlE347C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                          TIGREAMS; TIGRO0633; xth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                          117 ITWNIDGLDLNNLSERARGVCSYLALYSPDVIFLQE--VIPPYYSYLKKRSSNYEIITGH 174
 225
                                                                175
                                 59
                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: MONOMER (BY SIMILARITY).
SIMILARITY: BELONGS TO THE AP/EXOA FAMILY OF DNA REPAIR ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: progressively in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphates.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration {f \cdot} en the Swiss Institute of Bioinformatics and the EMBL outstation {f \cdot}
 SHLESTRGHAAERM-NQLKMVLKKMQEAPESATVIFAGDTNLRDREVT--
                                OKGHYGVALLTKQEPKV-IRRGFPTDNEDAQKRIIMADLE---TEFGLLTVINGYFPQGE
                                                              EEGYFTAIMLKKSRVKLKSQEIIPFPSTKMMRNLLCVHVNVSGNELCLMT--
                                                                                                                                                              l Similarity
59; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       equires a license agreement (Semail to license@isb-sib.ch).
                                                                                                                                                              Conservative
                                                                                                -LRARPHQLEATIEKYQPDVIGLQEIKVADEAFPYEITENLGYHVFHHG
                                                                                                                                                                             5.4%;
21.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Degradation of doul 3'-to 5'-direction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EC 3.1.11.2) (Exonu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma
                                                                                                                                                              45;
                                                                                                                                                                             Score 102.5; D
Pred. No. 0.34;
                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMIDINIC ENDONUCLEASE OF E.COLI.
TOSINES AND GUANINES BY CLEAVING
A BETA-ELIMINATION REACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   double-stranded DNA. It a
ion, releasing nucleoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Exonuclease III) (EXO
                                                                                                                                                                                              DB
                                                                                                                                                              108;
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                                                                                                                                                                                              1;
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                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restrictions
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                                                                                                                                                                                              267;
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for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acts
e 5′-
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G6PI_SA
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                                                             Query Match
Best Local
                                                Matches
                                                                                               ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Creace,
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI)
                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commentities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Schenberg M., Rutherford K., Simmonds M., Skelton J., Stevens K., White M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                     PRINTS; PR00662; G6PISOMERASE.

PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.

PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.

Isomerase; Gluconeogenesis; Glycolysis; Complete
RCT_SITE 386 386 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SALTI
                                                                                                                                                                                          InterPro; IPR001672; G6P_Isomerase
                                                                                                                                                                                                         EMBL; AL627282; CAD09205.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Whitehead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGI OR STY4417.
Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8Z1U7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G6PI_SALTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115
  51
                          85
                                                                                                                                                                                                                                 send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                   phosphate.

PATHWAY: Involved in glycolysis and in gluconeogene SUBUNIT: Homodimer (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

STHEATTY: BELONGS TO THE GPI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: D-glucose 6-phosphate =
                     VDLTNEETTDSTTSKISPSEDTQQENG-----SMFSLITWNIDGLDLNNLSERARGVCS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIDHILVSQKLAERCVDVGIALDIRAMEK-----PSDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFDRIFF-RAAAEEGHIIPRSLDLLGLEKLDCGRFPSDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---RCGGLPN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTGKCSFLPEERAWYQRLYDYGLEDSFRKLNPTANDKFSWFDYRSKGFDDNRG-----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRAHETKFPAKEKFYADLQQYLEK--EHDKSNPILIMGDMNISPSDLDIGIGDENRKRWL 172
                                                                                                                                                                                  PF00342; PGI;
                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          S., Barrell B.G.;
                                                                                                 549
                                                                                                            386
514
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                               61414 MW;
                                                          5.4%;
21.3%;
 -QDLAKETDLAGAIKSMFS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -NIVDVWEFLGKPKHCQYTW----DTQMNSNLGITAACKL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gamma
                                        Pred. No. U.77
5; Mismatches
                                                                                                           BY SIMILARITY.
BY SIMILARITY.
                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                              3CFE39008185D56E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subdivision;
                                                                      102.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       549
                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                          .94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ā
                                                                                                                                                                                                                                                                                                                                                                gluconeogenesis
                                                                       ĎВ
                                               90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259
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                                                                                                                                                                                                                                                                                                                                                                                         D-fructose
-GEKINRTEDRA---VL
                                                                                                                               proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Phosphoglucose
                                                                      Length
                                             103;
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226
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                                                                                                                                                                                                                                                                              on
                                             18;
RESULT 11
G6PI_SALTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G6PI_SALTY
Q8ZKI4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277
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15-JUN-2002 (Rel. 41, Creacce, 15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI)
isomerase) (PGI) (Phosphohexose isomerase) (PHI).
                                                                                                                                                                                InterPro; IPRO01672; G Pfam; PF00342; PGI; 1. PRINTS: DBOOCCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., M Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nha Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                             EMBL; AE008897; AAL23045.1;
                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)-!- SIMILARITY: BELONGS TO THE GPI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 413:852-856(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphate.

PATHWAY: Involved in glycolysis and SUBUNIT: Homodiner (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEIIPFPSTKMMR----NLLCVHVNVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNNIVDVWEFLGKPKHCQYT-WDTQMNSNLGITAACKLRFD---RIFFRAAAEEGHI---
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Best Local :
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01-NOV-1997
16-OCT-2001
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                                                                                                                between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6)
beta chain) (RNA polymerase beta subunit).
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                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete sequence analysis of the genome pneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma pneumoniae Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPOB OR MPN516 OR MP326.
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                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herrmann R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Himmelreich R., Hilbert H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2104;
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CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
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Best Local
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P09599;
01-MAR-1989
01-MAR-1989
15-JUN-2002
                                                                                                                                                                                                                                                                                            Johansen T., Haugli F.B., Ikezawa H., Lit
"Bacillus cereus strain SE-1: nucleotide
sphingomyelinase C gene.";
Nucleic Acids Res. 16:10370-10370(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus cereus.
Bacteria; Firmicutes;
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Pfam; PF00562; RNA_POL_BETA; 1.

PROSSTIE; PS01166; RNA_POL_BETA; 1.

Transferase; Transcription; DNA-directed RNA polymerase;
                                                                                                 Kuzmin N.P., Gavrilenko I.V., Krukov V.M., "Nucleotide sequence of phospholipase C and from Bacillus cereus BKW-B164 (letter)."; Bioorg. Khim. 19:133-138(1993).
                                                                                                                                                                                          MEDLINE=93249510; PubMed=8387306;
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89057484; PubMed=2848222;
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  MEDLINE=88313678; PubMed=3137122;
                            STRAIN-SE-1
                                                SEQUENCE OF 1-188
                                                                                                                                                                                                                         STRAIN-VKM 164;
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1396;
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11-MAR-1989 (Rel. 10, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-hingomyelinase C precursor (EC 3.1.4.12) (Sphingomyelin
15-bhosphodiesterase) (SMase) (SMPLC) (Cereolysin B).
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                                                   FROM N.
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22.1%;
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Pred. No. 3.
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                                                                                                                                                                      Karpov A.V
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Best Local
                                                                     01-NOV-1995 (Rel. 32, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose isomerase) (PHI).
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        Bacteria;
                                                          PGI OR HI1576.
                                                                                                                                                                                           P44312;
01-NOV-1995
                                                                                                                                                                                                                                                G6PI_HAEIN
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EMBL; X12854; CAA31333.1; -.
EMBL; X1240; CAA45501.1; ALT_INIT.
EMBL; X61440; CAA45501.1; ALT_INIT.
PIR; S01950; S01950.
InterPro; IPR005135; Exo_endo_phos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for non-entities requires a license account.
                           Haemophilus influenzae
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SIGNAL 1 27
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"Cloning and sequencing of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 SPSEDTQQENGSMFSLITWNIDGLDLN-----NLSERAR--GVCSYLALYSPDVIFLQEV 153
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SIMILARITY: BELONGS TO THE NEUTRAL SPHINGOMYELINASE FAMILY.
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CATALYTIC ACTIVITY: Sphingomyelin +
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                                                                                                                                                                                                                                                                                                                                                                                ASIPSYTGHTATWDATTNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AERMNQLKMV--LKKMQEAPESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IQYVFAKGCGPDNLSNKGFVYTKIKKNDRFVHV-----IGTHLQAEDSMCGKTSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPPYYS----YLKKRSSNYEIITGHEEG-----YFTA-----IMLKKSRVKLK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVQADTSTDQNNTLKVMTHNVYMLSTNLYPNWGQSQRADLIGAADYIK--NQDVVILNEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FDNSASDRLLGNLKKEYPNQTAVLGRSNGNEWDKTLGSYSSSTPEDGGVAIVSKWPIVEK
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  Proteobacteria;
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333 AA;
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                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186
36949 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     303
                                                                                                                                                                                                                                                                                                                                                                                265
  gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 99.5; DB Pred. No. 0.81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPHINGOMYELINASE C. BY SIMILARITY.
                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              035EF97D690C8378
subdivision; Pasteurellaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATIONS FOR OF SPHINGOMY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H(2)0 = N-acylsphingosine +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENNSDSEYASMFKTLH
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ID PGCV_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isomerase;
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzbugh W., Fleids C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Meidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Eritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; Q9N1E2; 1HOX.
TIGR; HI1576; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphate.
-i- PATHWAY: Involved in glycolysis and in gluconeogenesis
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE GPI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                 159
                                                                                                                                                                                                                                                                                                           140 LAL----YSPDVIFLQEVIPPYYSYL-KKRSSNYEIITGHEEGYFTAIMLKKSRVKLKSQ
                                                                                                                                                                                                                                                                                99
                                                                                                                                                                                                                                                                                                                                                                           85 VDLTNEETTDSTTSKISP-----SEDTQQENGSMFSLITWNIDGLDLNNLSERARGVCSY 139
                                                                                                                                                                                                                                                                                                                                              51 IDFSKNNINQTTLSHLRQLAQECALDSAKE--AMFT
                                                                                LW----
                                                                                                               -WDTQMNSNLGITAACKLRF
                                                                                                                                                                                                                                            EIIPFPSTKMMR----NLLCVHV--NVSGNE----
                                                                                                                                                                         RMNQLKMVLKKMQEAPESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYT 296
                                                                                                                                                                                                           DLGPYMVTEALRPYKNHLNMHFVSNVDGTHIAETLKKVNPETTLFLVASKTFTTQETMTN
                                                                                                                                                                                                                                                                             TALRNRTNTPVLVDGKDVMPEVNAVLAKMKDFCQRIISGEWKGYTGKAITDVVNIGIGGS
                                                                                                                                              AQSARDWLLKAAKDESAVAKHFAALSTNAKD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U32831; AAC23219.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00662; G6PISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gluconeogenesis; Glycolysis; Complete 387 387 BY SIMILARITY. 515 515 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                549 AA;
                                                                              SAIGLSIALSIGFENFEALLNGAHEMDKHFLSTPIEQN--IPTTLALVGL
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61622 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                              5.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G6P_Isomerase
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                                                                                                                                                                                                                                                                                                                                                                                                               54;
                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 98.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F65348C667068F16 CRC64;
                                                                                                           ----DRIFFRAAAEEGHIIPRSLDLLGL
                                                                                                                                            -VEKFGIDTNNMFEFWDWVGG----RYS
                                                                                                                                                                                                                                              DВ
                                                                                                                                                                                                                                                                                                                                              -----GEKINRTENRA---VLH
                                                                                                                                                                                                                                                                                                                                                                                                               112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 549;
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                                                                                                                                                                                                                                                                              158
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STANDARD;

PRT;

3396

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P13611; P20754; Q9UNW5;
01-JAN-1990 (Rel. 13, C
01-NOV-1997 (Rel. 35, L
16-OCT-2001 (Rel. 40, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    versican
J. Biol.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Versican core protein precursor (Large fibroblast CChondroitin sulfate proteoglycan core protein 2)
hyaluronate-binding protein) (GHAP).
CSPG2.
                                                                                                                                                                                                                                                                           Genomics
[6]
TJSSUE-Brain;
MEDLINE-89174663; PubMed-2466833;
Perides G., Lane W.S., Andrews D.
"Isolation and partial characteri
                                                                                                                                                                                                Zako M., Shinomura T., Ujita M., Ito K., I "Expression of PG-M(V3), an alternatively without a chondroitin sulfate attachment:
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            Krusius T., Gehlsen K.R., Ruoslahti E.;
"A fibroblast chondroitin sulfate proteoglycan
lectin-like and growth factor-like sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dours-Zimmermann M.T., Zimmermann D.R.;
"A novel glycosaminoglycan attachment domain ide
alternative splice variants of human versican.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zimmermann D.R., Ruoslahti E.; "Multiple domains of the large fibroblast EMBO J. 8:2975-2981(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM V1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Naso M.F., Zimmermann D.R., Iozzo R.V.; "Characterization of the complete genomic structuration of functional analysis of its J. Biol. Chem. 269:32999-33008(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM VO).
MEDLINE=95105188; PubMed=7528742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                         MEDLINE=99327053; PubMed=10397680;
                                                                                                                                        SEQUENCE OF 3333-3396 FROM N.A. (ISOFORM VINT) TISSUE-Aortic smooth muscle;
                                                                                                                                                                                                                                                                                    "Mapping of the versican proteoglycan human chromosome 5 (5q12-5q14)."; Genomics 14:845-851(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Lung fibroblast;
MEDLINE=88007514; PubMed=2820964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-90059882;
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                                                                                                                 Lemire
                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                         McPherson J.D.;
                                                                                                                                                                                                                                                                                                                                            MEDLINE-93122792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95105187;
                                                     PARTIAL SEQUENCE
                                                                                        "Versican/PG-M
                                                                                                                                                                                                                                     MEDLINE=95181355; PubMed=7876137;
                                                                                                                                                                                                                                                                                                                                    Iozzo R.V.,
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                                                                                                      T.N.;
                                                                                                                J.M., Braun K.R.,
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                                                                                                                                                                                                                                                                                                                                                            OF 251-347 FROM N.A
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                                                                                                                                                                             Chem.
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                                                                               Thromb.
                                                                                        isoforms
                                                                                                                                                                            270:3914-3918(1995).
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                                                                                                                                                                                                                                                                                                                                             PubMed-1478664;
                                                                                                                                                                                                                                                               (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created
                                                                               Vasc.
      Andrews D., Dahl characterization
                                                                                                                                                                                                                                                                                                                                    Cannizzaro
                                                                             in vascular smooth muscle cells."; asc. Biol. 19:1630-1639(1999).
                                                                                                                 Maurel
                                                                                                                                                                                                                                                               V3).
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                                                                                                                 P.
                                                                                                                                                                                                                                                                                                                                   L.A.,
                                                                                                                Kaplan
                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain identified
                                                                                                                                                                                              iy spliced for t in record
     of,
                                                                                                                                                                                                                                                                                                                                    Wasmuth
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      Ω,
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     Bignami
a glial
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                                                                                                                                                                                                                                                                                                                                                                                                          core
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                                                                                                                 Schwartz
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(PG-M) (Glial
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PRESENTATION OF THE PRESEN
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EMBL; X1598; CAA34128.1; -.
EMBL; X25488; AAB24878.1; -.
EMBL; U2655; AAA67565.1; -.
EMBL; U32039; BAA06801.1; -.
EMBL; J02814; AAA36437.1; -.
EMBL; AF084545; AAA948545.1; -.
EMBL; A6084545; AAD48545.1; -.
PIR; A60314; S06014.
PIR; A39358; A30358.
PIR; A39358; A30358.
PIR; A39358; A30358.
PIR; A39358; A30358.
                      ProDom;
SMART; S
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SMART;
SMART;
                                                                                                                                                                                                                                               Pfam; PF PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hyaluronate-binding protein.";
J. Biol. Chem. 264:5981-5987(1989).
                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Differential expression of versican isoforms in brain J. Neuropathol. Exp. Neurol. 55:528-533(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE
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DEVELOPMENTAL STAGE: Disappears after the cartilage development.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

SIMILARITY: CONTAINS 2 LINK DOMAINS.

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.

SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ween the Swiss Institute of Bioinforma
European Bioinformatics Institute. The
by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SÜBCELLULAR LOCATION: Secreted; extracellular matrix. ALTERNATIVE PRODUCTS: At least 5 isoforms; VO (shown here), V2, V3 and Vint, are produced by alternative splicing. TISSUE SPECIFICITY: Cerebral white matter. VO and V1 is expanding the specific of the specific 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in normal brain, gliomas, neurofibromas, and mennir and gliomas; v3 is found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hyaluronic acid.
                                                                                                                                                                                                           ; PF00084; sushi; ; PF00193; Xlink; ; PF00010; EGFBLC ; PR000010; Link; ; pn000918; Link;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                v; HGNC:2464; CSPG2
118661; -.
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PF00047;
                                                                                       SM00032;
SM00034;
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SM00001;
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IPR001304;
IPR000538;
IPR000436;
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IPR003599;
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                                                                                18; Link; 2.; CCP; 1.; CLECT; 1.; EGF_CA; 1.; EGF_Like; 1
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Lectin_C.
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EGF-like.
EGF_2.
EGF_Ca.
EGF_II.
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PS00010;

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PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01241; LINK; 2.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi; Glycoprotein; Proteoglycan; Lectin; Emunoglobulin domain; Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
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IKKEESTKHFPKGMRP-----TIQESDTELLFSGLGSGEEVLPTLPTESVNFTEVEQIN 2280
                         LKKRSSNYEIITGHEEGYFTAIMLKKSRVKL-----KSQEIIP-----
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EGF-LIKE 2, CAL

C-TYPE LECTIN.

SUSHI.

BY SIMILARITY.

BY SIMILARITY
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Pred. No. 26;
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IG-LIKE V-TYPE
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ALIGNMENTS

hypothetical protein Y63D3A.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27272
R;White, S.

asparagine/asparta

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hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Dete: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B86252
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.;
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; De
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.;
CA.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; N
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.;
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A. Recession: B86252
                                                                                                                      A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-502 <WOO>
A; Cross-references: EMBL:AL049769; PIDN:CAB42372.1; GSPDB:GN00067; SPDB:SPAC9B6.11c
                                                                                                                                                                                                                                                                                                                                              C; Access
R; Wood,
                                              A; Map position:
A; Introns: 76/1
C; Superfamily: :
                                                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDB:
                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: T40792
                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data A; Reference number: Z21875
                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein SPAC9B6.11c - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe
C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000
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A; Map position: 1
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A; Residues: 1-441 <STO>
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                                           ;Superfamily:
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Best Local
Query
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Match
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                                                                                                                                                                                                                                                                                                                           V.; Rajandream, M.A.; Barrell, B.G.; ad to the EMBL Data Library, May 1999
                                                                                                                 SPDB:SPAC9B6.11c
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                                           Schizosaccharomyces pombe hypothetical protein SPAC9B6.llc
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Pred. No. 6.9e-11;
  Score 113;
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  DB
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.S.; Maiti, R.;
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k;rinan, T.M.; Weldner, S.; Wong, K.; Buhrmester, J.; Chair, P.; Vorholter, F.J.; H. Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing A;Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: D95853
                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-252 KUR>
A; Residues: 1-252 KUR>
A; Cross-references: GB:AL591985; PIDN:CAC48492.1; PID:g15139964; GSPDB:GN00167
A; Experimental source: strain 1021, megaplasmid pSymB
R; Experimental source: strain 1021, megaplasmid pSymB
R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chain, P.; Cowle, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
                                                                                                                                                         A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidher, S.; Wells, D.H.; Wong, K.; A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                             L.; Hyman, R.W.; Jones, T
Science 293, 668-672, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: D95853
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                                                                 plasmid
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  Score 111.5; D
Pred. No. 0.15;
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5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
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```

Matches

Conservative

36; Mismatches

96;

Indels

57;

Gaps

12;

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R:Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; submitted to the EMBL Data Library, August 1999 A;Reference number: Z21580
                               hypothetical protein SC6E10.19c - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_C; Accession: T35506 R; Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barr
                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apurinic/apyrimidinic(AP)-endonuclease class II - slime mold (Dictyostelium discoideum) c;Species: Dictyostelium discoideum C;Species: Dictyostelium discoideum C;Date: 06-Dec.1996 #sequence_revision 13-Mar-1997 #text_change 18-Feb-2000 C;Accession: S68268 R;Freeland, T.M.; Guyer, R.B.; Lipey, N.-S.; Deering, R.A. Nucleic Acids Res. 24, 1950-1953, 1996 Nucleic Acids Res. 24, 1950-1953, 1996 A;Title: Apurinic/Apyrimidinic (AP)-endonuclease from Dictyostelium discoideum: cloning, A;Reference number: S68268; MUID:96226184; PMID:8657579
                                                                                                                                                                                                                                                                                                                              밁
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S68268
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A; Residues: 1-361 <F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: $68268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Cross-references: EMBL:U31631; NID:g1215675; PIDN:AAC47024.1; PID:g967268;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1995;Superfamily: exodeoxyribonuclease III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                           217
                                                                                                                                                                                                                           230
                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                               125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  α
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                                                                                                                                                                                                                     TRGHAAERMNQLKMVLKK------MQEAPESATVIFAGDTNLRDREV
                                                                                                                                                                                                                                                            GTGVLTKKK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLLAELDVVM 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TFPSRLPL----LRID-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRG-----LQRLDYRIKEWDVDFQAYLEKLNATKPIIWCGDLNVAHTEI
                                                                                                                                                                                                                                                                                        -TAIMLKKSRVKLKSQEIIPFPSTKMMRNLLCVHVNVSGNELCL-----
                                                                                                                                                                                                                                                                                                                        K----SVLSKGFTECVEKENPDVLCLQETKINP--SNIKKDQMPKGYEYHFIEADQKGHH 169
                                                                                                                                                                                                                                                                                                                                                        DLNNLSERARGYCSYLALYSPDVIFLQEV-IPPYYSYLKK----RSSNYEIITGHEEGYF 179
                                                                                                                                                                                                                                                                                                                                                                                           KAAAKKKSK--DEDEDEEEKEEEEETNKTTASVSIAIDNLDEPKVEENOMKIISWNVAGF 115
                                                                                                                                                                                                                                                                                                                                                                                                                         ESALERRPETISEPKTYVDLTNEETTDSTTSKISPSEDTQQE---NGSMFSLITWNIDGL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEEKEEVEEE-EEEDKKRKLVKKTPAKKA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGGREAAEEEGEPEVKKRRLLCVEFASVASCDAAVAQCFLAENDWEMERALNSYFEPPVE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QMNSNLGITAACKLRFDRIFFRAAAEEGHIIPRSLDLLGLEKLDC-----GRFPSDHW 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLKK---MQEAPESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLG-KPKHCQYTWDT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---TALPMRLIKAAPLPSSSEPRGALWVEIDVAAVKLQVIVTHL-GLRG--AERLRQATA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKKSRVKLKSQEIIPFPSTKMMRNLLCVHVNVSGNELCLMTSHLESTRGHAAERMNQLKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAAVIAECQPDVIALQEVDVGRARTGGIDQAHMIATHLNMEAEFHPALHLEDEKYGDAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-361 <FRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.8%; Score 110.5; Di
21.5%; Pred. No. 0.31;
                                                                                                                                                                                                                                                       -----PNAITFGIGIAKHDN-EGRVITLEYVQFYIVNTYIPNAG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HVLVGK--
                                                                 05-Nov-1999 #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94;
                                   Barrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                       260
                                                                                                                                                                                                                       270
                                                                                                                                                                                                                                                                                        -MTSHLES--
                                   B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------PAK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not
                                   Rajandream,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239
                                                                                                                                                                                                                                                                                        229
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                                   Z
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S50477
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                                                                                                                                                                                                                                                  Qy
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A; Residues: 1-477 <DIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
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R; Dietrich, F.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-253 <SEE>
                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                       1 Similarity
78; Conserv
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A;Gene: SGD:ISC1; MIPS:YER019w
A;Cross-references: SGD:S0000821
A;Map position: 5R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: The sequence of A;Reference number: S50433 A;Accession: S50477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein YER019w - yeast (Saccharomyces C;Species: Saccharomyces cerevisiae C;Date: 28-May_1993 #sequence_revision 24-Feb-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AL109661; PIDN:CAB51973.1; GSPDB:GN00070; A;Experimental source: strain A3(2) C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, December A; Description: The sequence of S. cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL:U18778; NID:g603592; PID:g603611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: T35506
A;Status: preliminary; translated from
190 HAPYAKQGDAAYLCHRSCQAWDFSRLIKLYRQA--GYAVIVVGDLN-----
                                                                                                                                        181 --AIMLKKSRVKLKSQEIIPFP-----
                                                                                                                                                                                                                                                                                      13 KEDGQSEFEALNGTNAIMSDNSKAYSIKFLTFNTWGLKYVSKHRKERLRAIADKLAGHSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCOEDB:SC6E10.19c
                                                                                                                                                                                                                                                                                                                     EETTDSTTSKISPSEDTQQENGSMFSL--ITWNIDGLDL--NNLSERARGVCSYLALYSP 145
                                             E---STRGHAAERMNQ-----LKMVLKKMQEAPESATVIFAGDTNLRDREVTRCGGLPN 278
                                                                                           GLAIL---SKVPIESTFLYRFPINGRPSAVFRGDWYVGKSIAITVLNTGTRPIAIMNSHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAVVRIGGARIGVLSSHLSL---DADERHEQAGLLLDHL-AALGVKHAVAGGDLNERPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPYYSYLKK-----RSSNYEIITGHEEGYFTAIMLK-KSRVKLKSQEIIPFPSTKMMRNL
                                                                                                                                                                                        LTPISDELLPNGGDSNENEDYDVIALQEIWCVEDWKYLASACASKYPYQRLFHSGILTGP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GHIIPRSLDLLGLEKLDCG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRTFRRLG---EGLRDCW--TAAPWGGEYTFP-----ATAPDRRIDAVFVTE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DREVTRCGGLPNNIVDVWEFLGKPKHCQYTWDTQMNSNLGITAACKLRFDRIFFRAAAEE 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LCVHVNVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQEAPESATVIFAGDTNLR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PREFRWRKKITRLAAAGDLVLLSGGGTAAGPALLCSLRATVERTEDVLLPLTPGRHRRGI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATSLPALPNSRTEPDGSAVIRVLSYNI-----RSLRDDTDALARVIKACAPDLVLLQEA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STTSKISPSEDTQQENGSMFSLITWNIDGLDLNNLSERARGVCSYLALYSPDVIFLQEVI 154
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --GIEVLGCGVPSGLAGVAEDDLRAATDHLPVLTALRV 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.7%;
19.5%;
                                                                                                                                                                                                                                                                                                                                                                                                             5.7%;
22.0%;
                                                                                                                                                                                                                                      -----DVIFLQEV-IPPYYSYLKKR-SSNYEIITGHEEGYFT-- 180
                                                                                                                                                                                                                                                                                                                                                                                         47;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 108; DB 2; Pred. No. 0.74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 108; DB Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----RFPSDHWGLLCNLDI
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB/EMBL/DDBJ
                                                                                                                                        -STKMMRNLLCVHVNVSGNELCLMTSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cosmids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9537,
                                                                                                                                                                                                                                                                                                                                                                                       Indels 106;
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241
                                                                                             189
                                                                                                                                           227
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RESULT 8
D90737
D90737
hypothetical protein ECs0868 [imported] - Escherichia coli (strain O157:H7, substrain C; Species: Escherichia coli
C; Species: Escherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C; Accession: D90737
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Accession: D90737
A; Molacule type: DNA
A; Residues: 1-253 <HAY>
A; Residues: 1-253 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAB34291.1; PID:g13360327; GSPDB:GN00154
A; Genetics:
A; Gene: ECs0868
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 01 A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: E85587 A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-253 <STO> A;Cross-references: GB:AE005174; NID:g12513779; PIDN:AAG55161.1; A;Cross-references: STrain O157:H7, Substrain EDL933 C;Genetics:
                                                                                                                                                                                                                               RESULT 9

RESULT 9

RESCHETION

Apportmentical protein ybhP [imported] - Escherichia coli (strain O157:H7, substrain C:Species: Escherichia coli
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: E85587
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Maller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apo Nature 409, 529-533, 2001
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Best Local S
Matches 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---IPPYYSYLKKRSSNYEIITG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KANHPLKVQAG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLKMVLKKMQEAPESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWDT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVSVDGAEKRGVLYCRIVP-PMTGKAIHVMCVHLGL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACRLDYALIDPDFLQTVDAGVRFTER-----IPHLDCS--VSDHFAYSCTLNIV 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACKLRF----DRIFFRAAAEEGHIIPRSLDLLGLEKLDCGRFPSDHWGLLCNLDII 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KFLTQEAGLVDSWEQLHGKQDLAVIARLSPLQQLLKGCTTCDSLLNTWRAQRQPD----E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----IIPFPSTKMMRNLLCVHVNVSGNELCLMTSHLESTRGHAAERMN 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 20.8 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LDEIFTRAHGRPARTFPVQFPLLRLDRI 220
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20.8%; Pred. No. 0.4;
Live 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----HEEGYFTAIMLKKSRVKLKSQE-- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -KHCQ-----YTWDTQMNSNLGITA
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                                                                        GSPDB:GN00145;
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R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; B. A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F64815
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F64815
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Best Local Similarity
Thehes 59; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ybhP protein - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep
C;Accession: F64815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-253 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: nucleic acid sequence
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                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                            Query Match
182
                                 300
                                                                   153
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                                                                                                                                                                                                                              154 ---IPPYYSYLKKRSSNYEIITG-----
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                                                                                                                                                                                                                                                                        3 DQTQQFS---FKVLTINIHKGFTAFNRRFILPELRDAVRTV-----SADIVCLQEVMG
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 KANHPLKVQAG----LDEIFTRAHGRPARTFPVQFPLLRLDRI
                                 QMNSNLGITAACKLRFDRIFFRAAAEEGHIIPRSLDLLGLEKL
                                                                                                   QLKMYLKKMQEAPESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWDT 299
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                                                                   QLAMLAEWVNELPDGEPVLVAGDFN---
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                                                                                                                                                                                                                                                                                                                                                            5.5%;
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                                                                                                                                                                                                                               ------HEEGYFTAIMLKKSRVKLKSQE-- 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82;
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                                                                                                                                     -REAHRQA
                                                                     --- DWRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -DWRQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                     181
                                                                                                                                     152
                                                                                                                                                                                                                                                                            52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V.; Riley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52
                                                                                                                                                                                                                                                                                                            153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PID:g17870
                                                                                                                                                                                                                                                                                                                                               11;
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X

RESULT T46340

11

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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 199

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Reference number: A84888
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein DKFZp434B0814.1 - human (fragment) C;Species: Homo sapiens (man) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #tex:Occession: T46340 R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; submitted to the Protein Sequence Database, January 2001
                                                                                                          A; Molecule type: DNA
A; Residues: 1-1374 <5T0>
A; Cross-references: GB: AEC02093; NID: g2583130;
C; Genetics:
                                                                                                                                                                                                                                                                                                                                    hypothetical protein At2945230 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: A84888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:AL137268
A;Experimental source: adult testis; clone DKFZp434B0814
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, January 2000 A;Reference number: 223037
A;Accession: T46340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-673 <AAA>
                                                                        A; Gene: At2g45230
A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           474 LYQRKLQAPLWPSSLGITDCCQ 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420 VARLSDGSHCPIILCGDLNSVPDSPLYNFIRDGEL-QYHGMP-----AWKVSGQEDFSHQ 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 VEGSMWAAIPMQSEPQ------YADC-AALPVGALATEQWEEDPAVLAWSIAP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 LEGGREAA-EEEGEPEVKKRRLLCVEFASVASCDAAVAQCFLAENDWEMERALNSYF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKFZp434B0814.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TWDTQMN-----SNLGITAACK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLITWNIDGLDLN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELLNRDNVGLVLLLQPLVPEGLGQVSVAPLCVANTHILYNPRRGDVKLAQMAILLAEVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLMSYNILAQDLMQQSSELYLHCHPDILNWNYRFVNLMQEFQHWDPDILCLQEVQEDHYW 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPVPQEEASIWPFEGLGQLQPPAVEIP--YHEILWREWEDFSTQPDAQGLKAGDGPQFQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP-PVEESAL -----ERRPETISEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQLEPSLRMMGFTCFYKRR-----TGCKTDG--CAVCYKPTRFRLLCASPVEYFRPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SYLKKRSSNYEIITG-HEEGYFTAIMLKKSRVKLKSQEIIPE--PST
1 Similarity
66; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -ESATVIFAGDTN------LRDREVTRCGGLPNNIVDVWEFLGKPKHCQY 295
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -LLCVHV-----NVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQE
                5.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.5%; Score 105.5; 1
20.4%; Pred. No. 1.9;
tive 62; Mismatches
36;
                  Score 105;
Pred. No. 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---NLSERARGVCSYLALYSPDVIFLQEVIPPYY- 158
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-Feb-2000 #text_change 04-Feb-2000
                                  DB
                                                                                                                              PIDN: AAB82639.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135;
                                  2;
98;
                                  Length 1374;
Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107;
                                                                                                                              GSPDB:GN00139
70;
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Gaps
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15;
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                                                                                                                              Вp
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                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                               Db
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                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                        맑
RESULT 14
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A;Molecule type: DNA
A;Residues: 1-281 < KUB;
A;Cross-references: GB:BA000019; PIDN:BAB75921.1;
A;Experimental source: strain PCC 7120
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakazaki, N.; Shimpo, S. DNA Res. 8, 205-213, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change C;Accession: AG2333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
AG2333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; Reference number: AB1807; MUID:21595285; PMID:11759840 A; Accession: AG2333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: alr4222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein alr4222 [imported] - Nostoc sp. (strain PCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
268
                                      350
                                                                               241
                                                                                                                                                                181
                                                                                                                                                                                                         245
                                                                                                                                                                                                                                                 126
                                                                                                                                                                                                                                                                                                                                                                           146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 LFPQA-KATYLQKI-C----SDHSPLINNL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 LKSQEIIPF----PSTKMMRNLLCVHVNVSGNELCLMT--SHLESTRGHAAERMNQLKMV 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 ELCLMTSHLESTRGHAAERMNQLKMVLKKMQEAPESATVIFAGDTNLRDREVTRCGGLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 VGH-LGFFDLHTVEPIGKSGGLALMWKDS-VQIKVLQ-----SDKRLIDALLIWQDKEFY 100
                                                                                                                                                                                                                                                                                                                                     77
                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 23.1 nes 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      27
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TNEETTDSTTSKISPSEDTQQE-NGSMFSLITWNIDGLDLNNLSE-RARGVCSYLALYSP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIVDVWEFLGKPKHC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ILSWNCQGVGNTPTVRHLRE-IRG------LYFPEVIFLCET------KKRRNYLENV
DHKPLLAEFTYI
                                    DHWGLLCNLDII
                                                                                                                                                                LHELELAISTHRGSILFAGDFNTWSRKRAVLLEKTVIRLGLKEAHFTPEENKKIKRFLLS
                                                                                                                                                                                                         LKKMQEA--PESATVIFAGDTN------LRDREVTRCG-----GLPNNIVDVWEFLGK 289
                                                                                                                                                                                                                                                 ATAKKYTYTKHHEPVFKTPKVSLITEYSLSHQQQTLLTINSHLIN----FVDLDKFKAQ
                                                                                                                                                                                                                                                                                                                                                                           DVIFLQEVIPPYYSYLKKRSSNYEIITG ------
                                                                                                                                                                                                                                                                                                                                                                                                                      TQELTIDS-----SQGLQTELNSNSIKVLNWNI---AKNNFEKFWFQDFFKILRLYQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IIPRSLDLLGLEKLDCGRFPSDHWGLLCNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KESSCLEFROMLNSCGLWEVNHSGYOFSWYGNRNDEL-----VQCRLDRTVANQAWME--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTCIYGEPVQAERGELWERLTRLGL-----SRSGPWMLTGDFNELVDPSEKIGGPAR
                                                                                                                       PKHCQYTWDTQMNSNLGITAACKLRFDRIFFRAAAEEGHIIPRSLDLLGLEKLDCGRFPS
                                                                                                                                                                                                                                                                                                                                     DIIFLQEV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nostoc sp.
279
                                      361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.5%;
23.1%;
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                                                                                                                                                                                                                                                                                                                                   -RMGVNVEQIMGETNMSWAYAPNFIDAHHQTY--SGILTAAKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 104.5; D
Pred. No. 0.66;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -QYTWDTQMNSNLGITAACKLRFDRIFFRAAAEEGH
                                                                               -LDYIFYRGLSEK----PATAKV--LDEI-CS---S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DВ
                                                                                                                                                                                                                                                                                                                                                                           ----HEEGYFTAIMLKKSRVK 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID:g17133357; GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamada,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S.; Watanabe, A.; Irigu
, M.; Yasuda, M.; Tabata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain PCC 7120
30-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                          349
                                                                                                                                                                                                                                                    180
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                                                                                 267
                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
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A;Cross-references: EMBL:Z81108; PIDN:CAB03235.1; GSPDB:GN00019; CESP:R09B3.1
A;Experimental source: clone R09B3
R;Tremblay, S.; Masson, J.Y.; Ramotar, D.
submitted to the EMBL Data Library, November 1997
A;Description: The exonuclease III family of DNA repair enzymes has a new homolog
A;Reference number: Z22150
A;Reference number: Z22150
A;Accession: T42391
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBL:AF034258; PIDN:AAC82328.1
C;Genetics:
A;Gene: R09B3.1
A;Introns: 83/3; 192/3; 264/3
A;Introns: 83/3; 192/3; 264/3
C;Superfamily: exodeoxyribonuclease III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ApD1115
Appothetical protein lmo0323 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AD1115
R;Glaser, P; Frangeul, L; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
R;Glaser, P; Frangeul, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D; Jones, L.M.; Karst, U.
D.; Jones, L.M.; Karst, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 294, 849-852, 2001
A; Aunthors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AD1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, October 1996 A; Reference number: Z19837 A; Accession: T24056 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-288 <WILL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exonuclease III homolog - Caenorhabditis elegans c;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: T24066; T42391
R;Kershaw, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: strain C; Genetics: A; Gene: 1mo0323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-256 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 GKFADSDGKQFYIFNTHLD----HISEEARLFASQLLLKKAATIAENSPVIILGDEN 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 --HVNVSGNELCLMTSHLESTRGHAAE--RMNQLKMVLKKMQEAPESATVIFAGDTN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 DWDYFGVGRDDGFEKGEFTAVFYNSTRFTLLQEGHFWLSETPDVPSIHSTAMFPR-ICVW 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S-NYEII---TGHEEGYFTAIMLKKSRVKL-----KSQEIIPFPSTKMMRNLLCV- 211
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45; Conservative
  47;
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Conservative
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25.4%;
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  33;
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                          Score 103; DB 2;
Pred. No. 0.91;
     Mismatches
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Voss, H.; Wehland
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                                                                                                                                                                           KKSRVKLKSQEIIPFPSTKMMRNLLC------VHVNVSGNELCLMTSHLESTRGHA 234
-KRGRWEKLLTEKMKEMDEKKPVIYGGDLNVAHNEI 189
                         AERMNQLKMVLKKMQEAPESATVIFAGDTNLRDREV 270
                                                    LSKCAPMKVHKGIGDPEFDTAGRLIIAEFSKFYFIGAYVPNSGAKLV----NLE-----
                                                                                                        RACVKKSDFKEVLAEEPDLVFLGETKCKEWPPEMEETFKNYTKTLVVSTEKNGGYAGVGL 104
                                                                                                                                  RA---RGVCSYLALYSPDVIFLQEV----IPPYYSYLKKRSSNYEIITGHEEGYFTAIML 184
                                                                                                                                                                  44
                                                                                                                                                                                            131
                                                         154
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Search completed: November 14, 2002, 10:28:15 Job time : 16.5673 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Comput
 Compugen Ltd
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Run OM protein protein search, using sw model

November 14, 2002, 10:23:41; Search time 29.293 Seconds (without alignments) 1646.697 Million cell updates/sec

Title: Perfect score: US-09-697-863A-2 1902 1 MELGSCLEGGREAA

MELGSCLEGGREAAEEEGEP......DCGRFPSDHWGLLCNLDIIL 362

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum Maximum DB DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 s summaries

A.Geneseq_101002:*

1: /SIDS2/gcgdata/ge
2: /SIDS2/gcgdata/ge
3: /SIDS2/gcgdata/ge
4: /SIDS2/gcgdata/s
5: /SIDS2/gcgdata/s
6: /SIDS2/gcgdata/s
7: /SIDS2/gcgdata/s
8: /SIDS2/gcgdat
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15: /SIDS2/gcgdat
16: /SIDS2/gcgdat
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18: /SIDS2/gcgdat
19: /SIDS2/gcg Database 1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT: *
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7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT: *
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score greater than or equal and is derived by analysis is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, of the total score distribution

Result	Score	Query Match Length DB	ength	DB	ID	Description
1			1 1 1 1	1		
بر	1902	100.0	362	21	AAY56019	Human CD40 recepto
2	1902	100.0	362	22	AAM39841	Human polymentide
ω	1902	100.0	372	22	AAM41627	Human polynentide
4	1902	100.0	392	20	AAY03182	Tonoisomerase II b
ر ت	1894	99.6	369	21	AAB53403	Human colon cancer
O	1893	99.5	362	22	AAB93674	Human protein sequ
7	1609	84.6	306	20	AAY03181	Topoisomerase II h
8	1258	66.1	370	21	AAY56020	Mouse CD40 recento
9	1199	63.0	263	22	ABG22067	Novel human diagno
10	1150.5	60.5	311	22	ABG22068	Novel human diagno

10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10			10		12									
4.5	5	4.5	4.5	4.5	4.5	4.5	. 5	4.5	4.5	4.5	ت. ت	5. 5	.5 .5	5.5	5	5		Б	5		106	106	109.5	111	7.5	169	231	231	231	231	231	231	376	837
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ALIGNMENTS

1	X	DT	XX	AC	XX	ID	AAY5	RESULT	
		15-MAR-2000 (first		AAY56019;		AAY56019 standard; Protein;	AAY56019	LT 1	
		(first entry)				Protein;			
•						362 AA.			
						AA.			

Human CD40 receptor associated protein.

Antiarteriosclerotic; antiarthritic; neuroprotective; dermatological; Immunosuppressive; antiinflammatory; immunosuppressive; antiallergic; human; CD40 receptor associated protein; CRAP; cytoplasmic domain; tumour necrosis factor; TNF; receptor; superfamily; CD30; homology; TNF receptor associated factor; TRAF; modulator; signalling pathway; diagnosis; NF-kappaB; Jun; kinase; atherosclerosis; multiple sclerosis; arthritis; systemic lupus erythematosus; graft rejection; allergy; graft versus host disease; autoimmune disease.

Homo sapiens

W09955859-A2

04-NOV-1999

28-APR-1999; 99WO-EP03025

29-APR-1998;

(VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG 98EP-0201392

Remacle JEFJG, Huylebroeck DFE;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the human CD40 receptor associated protein (CRAP). CRAP is a functional protein capable of interacting with the cytoplasmic domain of CD40 and/or other receptors of the tumour necrosis factor (TMF) receptor superfamily such as CD30 and TMF receptor I, where the protein has no homology to TMF receptor associated factor (TRAF) proteins. The CD40 binding proteins can be used as modulators of the CD40 signalling pathway, especially to diagnose and treat TRAF-related, CD40-related, NF-kappaB related and/or Jun (kinase)-related diseases, and for the improvement of anti-tumour diseases. Diseases which may be treated include atherosaclerosis, arthritis, multiple sclerosis, systemic lupus erythematosus, graft rejection, graft versus host disease, allergy, and autoimmune disease. The proteins can be used to sensitize tumour cells to anti-timour treatments and treases.
Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells to anti-tumour treatments and to screen for compounds which interfere with the interaction of the proteins with other protein components of the TRAF, CD40 or NF-kappaB related pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-062029/05
N-PSDB; AAZ47119.
                                                                                      22-OCT-2001
                                                                                                              AAM39841;
                                                                                                                                    AAM39841 standard; Protein;
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                                                               polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Page 39-41; 48pp; English.
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Pred. No. 3.2e-188;
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Query Match
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Matches 362
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
13-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                         Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, and thrombolytic activity, cancer diagnosis and therapy.
                                                                                                                                                                                                                                                                                                           immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang
Wang
Zhao
                                                                                                                                                                                            assays for receptor activity, arthritis and C.N.S disorders.
                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) the encoded polypeptides (AAM38642-AAM42213) with nootropic,
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29-NOV-2000;
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MELGSCLEGGREAAEEEGEPEVKKRRLLCVEFASVASCDAAVAQCFLAENDWEMERALNS
            MELGSCLEGGREAAEEEGEPEVKKRRLLCVEFASVASCDAAVAQCFLAENDWEMERALNS
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2000US-0727344.
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Pred. No. 3.2e-188;
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IDGLDLNNLSERARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSSNYEIITGHEEGYFT

AIMLKKSRVKLKSQEIIPFPSTKMMRNLLCVHVNVSGNELCLMTSHLESTRGHAAERMNQ

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YFEPPVEESALERRPETISEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWN 120

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       The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polypucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombourties activity, chemotactic/chemokinetic activity, haemostatic and thrombourties.
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19-OCT-2000;
29-NOV-2000;
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19-JUL-2000;
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25-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                                                                Novel nucleic acids and polypeptides, useful for treating such as central nervous system injuries -
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9-OCT-2000;
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DB; AAI60783.
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Xue AJ,
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Note: The sequence data for this patent
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                                                                    WPI; 1999-257704/22.
N-PSDB; AAX28153.
                                                                                                                                                                                                                                                                                         Topoisomerase II binding protein
                                              New Topoisomerase II-
                                                                                                                                                                                            23-MAR-1999
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                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                          AAY03182;
                                                                                                                                                                                                                                                                                                                                                                 AAY03182 standard; protein;
                                                                                                       (CHUS ) CHUGAI PHARM CO (TSUR/) TSURUO T.
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Claim

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Page 13-14;

28pp; Japanese

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RESULT 5
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N-PSDB; AAC98160
                                                                                Rosen CA,
                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                            12-MAR-1999;
                                                                                                                                                                                                                                           08-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder, infectious disease; cardiovascular disorder.
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                                                                                                                                                                                                                                                                                                  21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                       WO200055351-A1
                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identification; cytostatic; cardioactive; neuroprotective; vulnerary;
immunomodulatory; muscular; gynaecological; gastrointestinal;
nephrotropic; antiinfective; antibacterial; gene therapy; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human colon cancer antigen protein sequence SEQ ID NO:943.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colon cancer; colon cancer antigen; diagnosis; detection;
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Claim 11; Page 1508-1509; 2104pp;
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human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins system disorders, muscular diseases such as neural disorders, immune system disorders, wounds, renal disorders, intectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present invention. AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The invention

Sequence 369 AA;

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Pred. No. 2.2e-187;
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26-JUN-2001

(first

entry)

protein

sequence SEQ ID NO:13210.

detection; diagnosis; antisense therapy; gene therapy

AAB93674;

AAB93674 standard; Protein; 362

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02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                       the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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27-AUG-1999;
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LKMYLKKMOEAPESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWDTQ
                                                                                                                                                                                                    YFEPPVEESALERRPETISEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWN 120
                                                                  AIMLKKSRVKLKSQEIIPPPSTKMMRNLLCVHVNVSGNELCLMTSHLESTRGHAAERMNQ
                                                                                                                                    IDGLDLNNLSERARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSSNYEIITGHEEGYFT
                                                                                                                                                                                      CFEPPVEESALERRPETISEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWN
                                                                                                                  IDGLDLNNLSERARGYCSYLALYSPDVIFLQEVIPPYYSYLKKRSSNYEIITGHEEGYFT
                                                                                                                                                                                                                                                      MELGSCLEGGREAAEEEGEPEVKKRRLLCVEFASVASCDAAVAQCFLAENDWEMERALNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s
                                                 AIMLKKSRVKLKSQETIPFPSTKMMRNLLCVHVNVSGNELCLMTSHLESTRGHAAERMNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                        361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isogai T,
3, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                          present invention.
                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID 13210;
                                                                                                                                                                                                                                                                                                                                                                                            362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                        Conservative
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99JP-0300253
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T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                      99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2537pp + CD ROM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wakamatsu
                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                        Score 1893; DB 22;
Pred. No. 2.8e-187;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saito K, Y
, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto
                                                                                                                                                                                                                                                                                                                                                          362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a combination
                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                        Gaps
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AAY03181
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В
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Best Local S
                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY03181;
                                                                                                                                                                                                                                                                            This sequence represents the topoisomerase II binding protein (TopBP) of the invention. The TopBP protein is useful as an anticancer agent. TopBP can be used as the target molecule for anticancer agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY03181
                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                          Claim 1; Page 12-13;
                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-257704/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP11075856-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Topoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Topoisomerase II binding protein
                                                                                                                                                                                                                                                                                                                                                         New Topoisomerase II- binding protein - useful as
                                                                                                                                                                                                                                                                                                                                                                                                   (CHUS ) CHUGAI
(TSUR/) TSURUO
                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 LKMYLKKMQEAPESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWDTQ
241
                     297
                                         181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MNSNLGITAACKLRFDRIFFRAAAEEGHIIPRSLDLLGLEKLDCGRFPSDHWGLLCNLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IL 362
                                                                                  GYFTAIMLKKSRVKLKSQEIIPFPSTKMMRNLLCVHVNVSGNELCLMTSHLESTRGHAAE
                                                                                                                                      TWNIDGLDLNNLSERARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSSNYEIITGHEE 176
                                                                                                                                                                                  ALNSYFEPPVEESALERRPETISEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSL
                                                     RMNQLKMVLKKMQEAPESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYT
                                                                                                                           ITWNIDGLDLNNLSERARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSSNYEIITGHEE
                                                                                                                                                                      ALNSYFEPPVEESALERRPETISEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSL
 WDTQMNSNLGITAACKLRFDRIFFRAAAEEGHIIPRSLDLLGLEKLDCGRFPSDHWGLLC
                    WDTQMNSNLGITAACKLRFDRIFFRAAAEEGHIIPRSLDLLGLEKLDCGRFPSDHWGLLC
                                         RMNQLKMVLKKMQEAPESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYT
                                                                                                                                                                                                                 306;
                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                           306 AA;
                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          binding protein; TopBP; anticancer agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                          84.6%;
                                                                                                                                                                                                                                                                                                                           28pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 AA
                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                          Score 1609; DB 20 
Pred. No. 6e-158;
                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                       DB 20;
                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                             an
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                  Gaps
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                      356
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357

NLDIIL

362

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В
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                                                                                                                                                                                            CC This sequence represents the mouse CD40 receptor associated protein CC (CRAP). CRAP is a functional protein capable of interacting with the CC cytoplasmic domain of CD40 and/or other receptors of the tumour necrosis CC factor (TNF) receptor superfamily such as CD30 and TNF receptor I, where CC the protein has no homology to TNF receptor associated factor (TRAF) proteins. The CD40 binding proteins can be used as modulators of the CC CD40 signalling pathway, especially to diagnose and treat TRAF-related, CC CD40-related, NF-kappaB related and/or Jun (Kinase)-related diseases, and for the improvement of anti-tumour diseases. Diseases which may be treated include atherosclerosis, arthritis, multiple sclerosis, systemic Lipus erythematosus, graft rejection, graft versus host disease, allergy, cells to anti-tumour treatments and to screen for compounds which components of the TRAF, CD40 or NF-kappaB related pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                          Query Match
Best Local
                                                                                                           Matches
                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 41-43; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressive; antiinflammatory; immunosuppressive; antiallergic; human; CD40 receptor associated protein; CRAP; cytoplasmic domain; tumour necrosis factor; TNF; receptor; superfamily; CD30; homology; TNF receptor associated factor; TRAF; modulator; signalling pathway; diagnosis; NF-kappaB; Jun; kinase; atherosoclerosis; multiple sclerosis; arthritis; systemic lupus erythematosus; graft rejection; allergy; graft versus host disease; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antiarteriosclerotic; antiarthritic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY56020 standard; Protein; 370 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse CD40 receptor associated protein.
            72
                                           24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
ERRPETISEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWNIDGLDLNNLSE 131
                                                               EAAEEEGEPEVKKRRLLCVEFASVASCDAAVAQCFLAENDWEMERALNSYFEPPVEESAL 71
                                  EAAQAE-EDRVKRRRLQCLGFALVGGCDPTMVPSVLRENDWQTQKALSAYFELPENDQGW 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLDIIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-062029/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteins used to treat ses and for improvement
                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Remacle JEFJG,
                                                                                                                                                                         370 AA;
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306
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                                                                                                                     66.1%;
68.4%;
                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huylebroeck DFE;
                                                                                                                   Score 1258;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammatory diseases, NF-kappaB related
  of anti-tumor treatments -
                                                                                                       Mismatches
                                                                                                    ; DB 21;
2.1e-121;
hes 64;
                                                                                                    Indels
                                                                                                                                 Length 370;
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RESULT 9
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                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics. forensics. aene manning, identification of mutartions
                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                     Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAS86254.
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG22067 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 KLRFDRIFFRAAAEEGHIIPRSLDLLGLEKLDCGRFPSDHWGLLCNLDIIL 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 PDSTTVIFAGDTNLRDQEVIKCGGLPDNVFDAWEFLGKPKHCQYTWDTKANNNLRIPAAY 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a; chromosome mapping; gene mapping; gene therapy; forensic;
supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWDTQMNSNLGITAAC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KHRFDRIFFR--AEEGHLIPQSLDLVGLEKLDCGRFPSDHWGLLCTLNVVL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSQEIIPFPNTKMMRNLLCVNVSLGGNEFCLMTSHLESTREHSAERIRQLKTVLGKMQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSQEIIPFPSTKMMRNLLCVHVNVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RARGVCSCLALYSPDVVFLQEVIPPYCAYLKKRAASYTIITGNEEGYFTAILLKKGRVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSSNYEIITGHEEGYFTAIMLKKSRVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRQPPTSFKSEAYVDLTNEDANDTTILEASPS-GTPLEDSSTISFITWNIDGLDGCNLPE
                                                                                                                                                                                                                                                                               SEQ ID No 52426; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnostic protein #22058
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C,
                    forensics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang
disorders or other traits to assess biodiversity
                    gene mapping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263
                identification of mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of mutations to assess
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Note: The sequence data for this patent did not appear in the printer specification, but was obtained in electronic format directly from W
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                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
            polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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polynucleotides
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                                     invention relates to isolated polynucleotide (I) and probes, control of the following probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSSNYEIITGHEEGYFTAIMLKKSRVKLK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWDTQMNSNLGITAACK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQEIIPFPSTKMMRNLLCVHVNVSGNELCLMTSHLESTKGHAAERMNQLKMGLKKMQEAP
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                                                                                                                                                                                         2001-639362/73.
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Pred. No. 1
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tches 2;
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from WIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences
                                                                                           forensic; gene therapy; chromosome mapping; signal peptide; prostate; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostat
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                                                                                                                                                                                                    Human 5'
                                                                                                                                                                                                                                                                                                     AAY11868 standard; Protein;
                                                                                 thrombolytic;
                                                                                                                                                                                                                                  18-JUN-1999
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hes 242;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -IDGLDL-NNLSERARGYCSYLALYSPDVIFLQEVIPPYYSYLKKRSSNYEIITGHEEGY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YFEPPVEESALERRPETISEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTAIMLKKSRVKLKSQEIIPFPSTKMMRNLLCVHVNVSGNELCLMTSHLESTRGHAAERM 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YLMGLDLKQSVQRRARGVCSYLALXVLSLLFNSNV----
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                                                                                                                                                                secreted protein; EST; expressed sequence tag; diagnosis;
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                                                                                                                                                                                                                                    (first
                                                                                 anti-inflammatory; tumour inhibition
                                                                                                                                                                                                                                    entry)
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                      Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopolesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostat
reproductive hormone regulation;
thrombolytic; anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation and differentiation activity, haematopolesis regulating activity, tissue growth regulating activity, haematopolesis regulating are regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptides can be used for obtaining corresponding promoter activities into a membrane, or importing a nolveneride into a membrane.
                                                                                                                                                                                                                                                                                                                   18-JUN-1999
                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                               AAY12175;
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY12175 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 34; Page 595; 675pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDGLDLNNLSERARGYCSYLALYSPDVIFLQEVIPPYYSYL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YFEPPVEESALERRPETISEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWN
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                                                                                                                                                                                                                    EST secreted protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                            (first entry)
   anti-inflammatory; tumour inhibition
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Pred. No. 2.4e-78;
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Arabidopsis 17-OCT-2000 AAG26231;

thaliana

protein fragment SEQ ID NO: 30610.

(first

entry)

Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;

mapping;

gene

pathway;

termination

sequence

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MELGSCLEGGREAAEEEGEPEVKKRRLLCXEFXSVASCDAAVAQCFLAXNDWEMERALNS

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YFEPPVEESALERRP

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YFEPPVEESALERRP 75

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AAG26231 standard; Protein;

404

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RESULT 13

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Query Match
Best Local
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                                                                                                                                                                    nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/chemokinetic activity, haematory activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion
                                                                                                                                                                                                                                                                                                                                                                     human secreted proteins, and encode the proteins given in AAV01602 and AAV11994 to AAV12260, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acids encoding human secreted proteins - obtained cDNA libraries prepared from kidney, fetal kidney, dystrophic muscle, muscle and heart tissue
                                                                                                                 Sequence
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Pred. No. 4.6e-31;
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S-0154039. S-0154779. S-0155139. S-0155486.

Arabidopsis thaliana protein fragment SEQ

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53080

18-OCT-2000

(first entry)

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RESULT 14
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                                                               113 MFSLITWNIDGLDLNNLSERARGVCSYLALYSPDVIFLQEVIPPYYSYLKKR-----
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                    217
                                    167
                                                       160
                                                    HLES-----
                 SVSVDVAVSRGYYCMLL---SKLGVKSFSSKSFGNSIMGRELSIAEVEVPGRKPLVFATS
                            NYEIITGHEEGYFTAIMLKKSRVKLKSQEIIPFPSTKMMRNLLCVHVNVSGNE-LCLMTS 225
                                                                                         84; Conservative
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-TRGHAAERMNQLKMVLKKMQEAPESATVIFAGDTNLRDREVTRCGG--
                                                                                       12.1%; Score 231; DB 21; 30.2%; Pred. No. 8.7e-15; tive 39; Mismatches 109;
                                                                                                           Length 426;
                                                                                         Indels
                                                                                         46;
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                                                                                         Gaps
275
                  273
                                                      216
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Db 274 HLESPCPGPPKWDQMFSRERVEQAKEAIEILR--PNANVIFGGDMNWCD----KLDGKF 326

Qy 276 -LPNNIVDVWEFLGKPKHCQYTWDTQMNSNLGITAACKLFEDRIFFR------ 321

Db 327 PLPDKWVDVWEVL-KPGDLGFTYDTKANPMLSGNRALQKRLDRILCRLDDYKLGGIEMVG 385

Qy 322 AAAEEGHIIPRSLDLLG-LEKLDCGRFPSDHWGLICNL 358

Qy 322 AAAEEGHIIPRSLDLLG-LEKLDCGRFPSDHWGLICNL 358

Db 386 KEAIPGLSYVKEKKVRGDIKKLELPVLPSDHFGLLVTL 423
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Search completed: November 14, 2002, 10:27:24 Job time: 31.293 secs

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Result
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                sp_phage:*
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sp_rvirus:*
sp_bacteriap:*
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5 Q9S2L9
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Q9rlv9 listeria iv
015921 trypanosoma
Q27811 tripneustes
Q9y7m8 schizosacch
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Q9nuk5 homo sapien
Q9d7n0 mus musculu
Q9xwg3 caenorhabdi
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ALIGNMENTS

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RESULT 1
Q9JJX7
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Qy
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Best Local S
Matches 370
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"TTRAP, a novel protein that associates with CD40, Tumor Necrosis Factor (TNF) Receptor-75 and TNF Receptor-Associated Factors (TRAFs), and that inhibits Nuclear Factor-kappaB activation.";
J. Biol. Chem. 275:18586-18593 (2000).
EMBL; AJ251328; CAB92971.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9JJX7 PRELIMINARY; PRT; 370 AA.
O9JJX7;
O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=20309820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Putative TRAF and TNF receptor associated protein TTRAP OR TTRAP.
                                                                                                                                                               Receptor.
                                                                                                                                                                               Pfam; PF03372; Exo_endo_phos;
                                                                                                                                                                                             MGD; MGI:1860486; Ttrap.
InterPro; IPR005135; Exo_endo_phos
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
                                                                                       Local Similarity nes 370; Conserv
61 NDWQTQKALSAYFELPENDQGWPRQPPTSFKSEAYVDLTNEDANDTTILEASPSGTPLED
                               Н
                            370 AA;
                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                              PubMed=10764746;
                                                                                                                                                  41033 MW;
                                                                                                    100.0%;
                                                                                         0,
                                                                                     Score 1968; DB 11;
Pred. No. 3.2e-168;
; Mismatches 0;
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                                                                                                                      DB 11;
                                                                                         Indels
                                                                                                                   Length
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                               60
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Query Match
Best Local
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"A novel gene expressed in human advenal gland. Submitted (JAN-2000) to the EMBL/GenBank/DDBJ of the EMBL/GenBank/DBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                      142
322 KHRFDRIFFR--AEEGHLIPQSLDLVGLEKLDCGRFPSDHWGLLCTLNVVL
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                                                            PESATVIFAGDINLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWDTQMNSNLGITAAC
                                                                                           PDSTTVIFAGDTNLRDQEVIKCGGLPDNVFDAWEFLGKPKHCQYTWDTKANNNLRIPAAY
                                                                                                                                                                      KSQEIIPFPNTKMMRNLLCVNVSLGGNEFCLMTSHLESTREHSAERIRQLKTVLGKMQEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF223469; AAF64144.1;
Pro; IPR005135; Exo_endo_phos; 1
PF03372; Exo_endo_phos; 1
:NCE 362 AA; 40956 MW; D6D6/
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Last sequence
Last annotation
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Pred. No. 1.6e:
43; Mismatches
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annotation
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EMBL; AL031775; CAA21141.1; -
EMBL; AJ269473; CAB92966.1; -
EMBL; AF201687; AAG35600.1; -
EMBL; BC017553; AAH17553.1; -
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DJ30M3.3 (TRAF and TNF receptor associated protein)
protein 2) (Hypothetical 40.9 kDa protein).
DJ30M3.3 OR TTRAP OR EAP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR005135; Exo_endo_phos. Pfam; Pf03372; Exo_endo_phos; 1. Receptor; Hypothetical protein. SEQUENCE 362 AA; 40929 MW; 3789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li R., Pei H., Papas T.S.;
"EAP2, a Novel Protein Interacting with ETS1.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
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                                                                 KSQEIIPFPSTKMMRNLLCVHVNVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQEA
                                                                                                                                               RARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSSNYEIITGHEEGYFTAIMLKKSRVKL
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T 01-JUN-2001 (TrEMBLrel. 17, Createu,
DT 01-JUN-2002 (TrEMBLrel. 17, Last sequence up)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation
DT 01-JUN-2002 (Tremblerel. 21, Last annotation)
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PF03372; Exo_endo_phos; 1.
NCE 362 AA; 40869 MW; 8E17
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
06 fis, clone PLACE1010031.
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68.1%;
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1249; DB 4
Pred. No. 1e-103;
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Q9XWG3
ID Q9XW
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RX MEDLINE-21085660; PubMed=11217851;
RX Kawai J., Shinagawa A., Shibatta K., Yoshino M., Itoh M., Ishii Y.,
RA Kawai J., Shinagawa A., Shibatta K., Yoshino H., Adachi J., Fukuda S.,
RA Arakwa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,
RA Arakwa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Kuehl P., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Hoffmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Kandone P., King B., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local S
Matches 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9XWG3;
01-NOV-1999 (TrEM
01-NOV-1999 (TrEM
01-JUN-2002 (TrEM
Y63D3A.4 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat.
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1860486; Ttrap.
InterPro; IPR005135; Exo_endo_phos.
Pfam; PF03372; Exo_endo_phos; 1.
SEQUENCE 157 AA; 17876 MW; 5920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 409:685-690(2001).
EMBL; AK009089; BAB26063.1; -.
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                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                   White
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                                                                                                                      MEDLINE=99069613;
                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLRDQEVIKCGGLPDNVFDAWEFLGKFKHCQYTWDTKANNNLRIFAAYKHRFDRIFFRAE
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157; Conser
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                                                                                                                                                                                                                                                                N.A.
                                                                                                                      PubMed=9851916
                                                                                                                                                                                                                                                                                                                                                Nematoda; Chromadorea; rinae; Caenorhabditis.
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12,
21,
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; Pred. No. 2.4e-68;
0; Mismatches 0;
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                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence up
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5920850802FAAE84 CRC64;
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Length 157; Indels

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Gaps

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   Theologis A.;
Submitted (MAY-1999) to the EMBL/GenBank EMBL; AC007296; AAD30241.1; -
EMBL; AC007296; AAD30241.1; -
InterPro; IPR001969; ASpprotease_site.
InterPro; IPR005135; Exo_endo_phos.
InterPro; IPR001876; Znf_RanGDP.
Rfam; pF03372; Exo_endo_phos; 1.
SMART; SMD0547; ZnF_RBS; 2.
                                                                                                                                                                 STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Li J., Lee J.M., Kremenetskaia I., Luros J., Ngan I., Liu A.,
Li J., Lee J.M., Kremenetskaia I., Luros J., Ngan I., Liu A.,
Gonzalez A., Altafi H., Araujo R., Conn L., Conway A.B.,
Dunn P., Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn P.,
Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"Arabidopsis thaliana chromosome I BAC F25C20 sequence.";
"submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9SA95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               investigating biology.";
Science 282:2012-2018(1998)
EMBL; AL032652; CAA21707.1;
                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                       STRAIN-CV.
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NPDILFLQEVVDRDLAPIDKLQSLYKIYYSNKGCQYYTAILVSK-MFDVEKHDVIHFQNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARSAAVMGASSSMASSGAAVMTAEDLKGFEVSVMSWNIDGLDGRSLLTRMKAVAHIVKNV
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113; Conser
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PS00141; ASP_PROTEASE; UNKNOWN_1.
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3372; Exo_endo_phos; 1.
362 AA; 40893 MW; 7899
                                                                                                                                       COLUMBIA;
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Last sequence update)
Last annotation updat
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Pred. No. 1.
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7895C47504866E52
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RX MEDLINE-20196006; PubMed=10731132;
RX MEDLINE-20196006; P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Dough L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Dough L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Dough L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Horris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Horris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Horris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.F., McPherson D.,
RA McNalon E., Kolsan K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Mount S.M., Welson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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Best Local
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01-MAY-2000
01-MAY-2000
01-JUN-2002
CG4796 prote
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Pterygota; Ne
Ephydroidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VPGRKPLVFATSHLESPCPGPPKWDQMFSRERVEQAKEAIEILR---PNANVIFGGDMNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGGNE-FCLMTSHLES-----TREHSAERIRQLKTVLGKMQEAPDSTTVIFAGDTNL
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441 AA;
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Neoptera; Endopterygota; Diptera;
a; Drosophilidae; Drosophila
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2 (TrEMBLrel.
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48995 MW;
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Last sequence
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6582FAA2D7BD0CA8
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annotation update)
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No. 3.4e-16;
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STRAIN-A3(2);
Seeger K., Harris D.;
Submitted (AUG-1999) t
[2]
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                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical protein SC02125.
SC02125 OR SC6E10.19C.
Streptomyces coelicolor.
                                                                                          Actinomycetales;
NCBI_TaxID=1902;
                                                                                                                                                                                                                                              Q9S2L9
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                                                                                                                           Bacteria; Firmicutes;
                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L-----STPALLQHVQ--QLRGGGIEQPSLLTRGFLKPLLADEDVADGLRCLKLNSVSR 107
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                                                                                                                                                                                                                                                                                                                       DR-LKIKNCLDFPAGEQIGKNRTPSFQYPSDHFSLVCDFELL 417
                                                                                                                                                                                                                                                                                                                                                     EEGHLIPQSLDL----VGLEKLDCGRFPSDHWGLLCTLNVV
                                                                                                                                                                                                                                                                                                                                                                                  DVKLDREEILHPNADVGEFVAKSMKREPPYT
                                                                                                                                                                                                                                                                                                                                                                                                              NV------FDAWEFLGK-----PKHCQYTWDTKANNNLRIPAAYKHRFDRIFFRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFYKRDKLQLQGYDTRILEVWRVQSNQVAIAARLRMRSSGREFCVATTHLKARHGALLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILLKKGRVKFKSQEIIPFPNTKMMRNLLCVNVSL----GGNEFCLMTSHLES------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VCSA----PVE-GDDIRLLQWNILSQTLGQHNDGFVRC--PEEALTWEHRKYLIVQEIL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -TREHSAERIRQLKTVLGKMQEAPDSTTVIFAGDTNLRDQE-----VIKCGGLPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF03372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR005135; Exo_endo_phos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449
                                 Harris D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Exo_endo_phos;
AA; 50275 MW;
                                                                                                          Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.4%;
20.8%;
                 6
                                                                                                        Actinobacteria; Actinobacteridae; ptomycineae; Streptomycetaceae; St
                 the EMBL/GenBank/DDBJ databases
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Pred. No. 0.0
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1607DF25A418A024 CRC64;
                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                              253
                                                                                                                                                                                                                                                                                                                                                                                  -TW----KIREEGEECHTIDYVFYTP
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                                                                                                           Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -VCSCLA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -TA 191
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RESULT 10
Q92X70
ID Q92X7
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                       Q92X70;

01-DEC-2001 (TrEMBLrel. 19, C

01-DEC-2001 (TrEMBLrel. 19, L

01-JUN-2002 (TrEMBLrel. 21, L

Hypothetical protein RB0092.

RB0092 OR SMB20092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=A3(2) / M145;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins I.

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth

Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor

Minarch T. Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL109661; CAB51973.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinashi H., Hopwood D.A.;

A set of ordered cosmids and a detailed the 8 Mb Streptomyces coedicolor A3(2) chwol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  James K.D., Parkhill Submitted (AUG-1999)
             Rhizobium meliloti (Sinorhizobium meliloti). Plasmid pSymB (megaplasmid 2). Bacteria; Protoobacteria; alpha subdivision; Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
SEQUENCE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF03372; Exo_endo_phos;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97000351; PubMed-8843436; Redenbach M., Kieser H.M., Denapaite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                Q92X70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro, IPR005135; Exo_endo_phos
                                                                                                                                                                                                                                                                                                                                                                                                                     57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSLPALPNSRTEPDGSAVIRVLSYNIRSLRD-DTDALARVIKAC----APDLVLLQEA-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TILEASP-SGTPLEDSSTISFITWNIDGLDGCNLPERARGVCSCLALYSPDVVFLQEVIP
                                                                                                                                                                                                                                                                   GHLIPQSLDLVGLEKLDCG-----
                                                                                                                                                                                                                                                                                                                                                          AAVVRIGGARIGVLSSHLSLDAD---ERHEQAGLLLDHL-AALGVKHAVAGGDLNERP--
                                                                                                                                                                                                                                                                                                                                                                                                                     RFFRWRKKITRLAAAGDLVLLSGGGTAAGPALLCSLRATVERTEDVLLPLTPGRHRRGIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYCAYLKK-----RAASYTIITGNEEGYFTAILLK-KGRVKFKSQEIIPFPNTKMMRNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                               GGRTFRRLGEGLRDCW--TAAPWGGEYTFPATAPD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 protein.
253 AA; 2
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                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                            -LPDNVFDAWEFLGKPKHCQYTWDTKANNNLRIPAAYKHRFDRIFFRAEE
                                                                                                                                                                                                                                         GIEVLGCGVPSGLAGVAEDDLRAATDHLPVLTALRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26691 MW; 1160CE2663C16622 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39;
                                                                                                                      Last
                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 118.5; DB 16;
Pred. No. 0.017;
9; Mismatches 115;
                                                                                                      Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the model
                                                                                                                                                                 PRT;
                             subdivision;
                                                                                                                      sequence update)
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hromosome.";
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                                                                                                    update)
                               Rhizobiaceae
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                                                                                                                                                                                                                                         249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taylor K.,
                             group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65;
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14;

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RESULT 11
ORDEP1
ID OBUEPA
C OBUEPA
C OBUEP
DT 01-JU
DT 01-JU
DT 01-JU
DT SAGTON
OC RAICO
OX NCBI_
RN [1]
RP SEQUE
RX WEDLI
RA Chapm
RA Ch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDILINE-21608550; PubMed=11743193;

WOOD D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo I

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Chapman P., Clendenning J., Datherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordc

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry
SEQUENCE FROM N.A MEDLINE=21608551;
                                                                                          Science 294:2317-2323(2001)
                                                                                                                                                                                             Gordon-Kamm B., Liao L., Kim S., Chumley F., Tingey S.V., Tomb J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel. Exonuclease III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATU1714 OR AGR_C_3151.
Agrobacterium tumefaciens
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Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 252 AA; 27376 MW; A8B6F2BC8A8316AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=1021;
MEDLIND=21396508; PubMed=11481431;
Finan T.M., Weidner S., Wong K., Buhrmester J.,
Vorhoelter F.J., Hernandez-Lucas I., Becker A.,
Golding B., Puehler A.;
                                                                                                                                                                            Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8UEP1;
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Proc. Natl. Acad. Sci. U.S.A. 98:9889-989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete sequence of the 1,683-kb pSymB megaplasmid fixing endosymbiont Sinorhizobium meliloti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHLIPQSLDLV--GLEKLDC-----GRFPSDHWGLLCTLNVVL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRDQEVIKCGGLPDNVFDAWEFLGKPKHCQYTWDTKANNNLRIPAAYKHRFDRIFFRAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMTSHLESTREHSAERIRQLKTVLGK---MQEAPDSTTVIFAGDTN--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSDAQLL-TGVKPRPTFPS--
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                                                                                                                                                                                          G., Saenphimmachak C., Wu Z., Romero P., Gordon
Tao Y., Biddle P., Jung M., Krespan W., Perry M.
Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.
yy S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
        PubMed-11743194;
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Pred. No. 0.072;
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Rhizobiaceae
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Best Local
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STRAIN-ATCC 19119;

MEDLINE-99348382; PubMed-10417642;

Gonzalez-Zorn B., Dominguez-Bernal G., Suarez M.,

Novella S., Vazquez-Boland J.A.;

"The smcL gene of Listeria ivanovii encodes a spi

mediates bacterial escape from the phagocytic vac

Mol. Microbiol. 33:510-523(1999).

EMBL; Y09477; CAA70683.2; -
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Science 294:323-3238(2001).
EMBL; AE009128; AAL42714.1; -. EMBL; AE00903; AAK87487.1; -.
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82 DVVILNEAFDTSASHRLLNNLREMYPHQTPVIGRSKHGWDKTEGNYSNFALEDGGVAVVS 141
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    PF03372; Exo_endo_phos; 1.
NCE     335 AA;     38455 MW;     46F3
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01-JAN-1998
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 015921
015921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99108141; PubMed=9889272;
Perez J., Gallego C., Bernier-Villamor V., Camacho A.,
Gonzalez-Pacanowska D., Ruiz-Perez L.M.;
"Apurinic/apyrimidinic endonuclease genes from the trypanosomatidae
leishmania major and Trypanosoma cruzi confer resistance to oxidizir
agents in DNA repair-deficient Escherichia coli.";
Nucleic Acids Res. 27:771-777(1999).
EMBL; U92486; AAD11456.1; -.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGR00195; exoDNase_III; 1.
TIGRFAMS; TIGR00633; xth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR004442; ExoDNase_III.
InterPro; IPR004808; ExoIII_xhi
InterPro; IPR005135; Exo_endo_phos.
Pfam; PF03372; Exo_endo_phos; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U92486; HSSP; P27695;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AP-endonuclease.
                                                                                                                                                                                                                                                                                                                                                                                       Endonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Euglenozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trypanosoma cruzi
  317
                           284
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                           GGL-PD-----
SGFTPEERASFRETLRVANAVDTFRALYPKAAPVYTFWSARINGRAR---GLGWRLDYFV
                                                                                                       TTYFGT - - QGKGSETFALALVNTYIPNSGMSLERLPYRCQKFDL - -
                                                                                                                                --YFTAILLKKGRVKFKSQEIIPF-PNTKMMRNLL---CVNVSLGGNEFCLMTSHLESTR
                                                                                                                                                                                         PPY----
                                                                                                                                                                                                              DSKHMLKFITWNVAGLRGL-LRKDDQAIQRLLEEEGPDALCLQETKLNPDDPQNEKLGEV
                                                                                                                                                                                                                                                                PPSRSLNSAGAEATSPNRPLAAVLTAPP---PSDDDTRKTEKDIWSQVEPFQRRTAAKDF
                                                                                                                                                                                                                                                                                          PPTSFKSEAYVDLTNEDANDTTILEASPSGTPLEDSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISKDTSRAIRAEQMQEIQTFIAK-KNIPKDEIIFIGGDLN-----VNYG--TDEYHDMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QWPIVEKSQHIFQRGGGADRLSNKGFAYVKIMKN-----
                                                                            EHSAERIRQLKTVLGKM-----QEAPDSTTVIFAGDTNLRDQE------
                                                                                                                                                           PGYRFVDHVCRAKKGYSGTRTYIKNTAAAEWKTVTVKGFDTLKSPQDVGHSEGDEEGRVL
                                                                                                                                                                                                                                       ----TISFITWNIDGLDGCNLPERARGVCSCLALYSPDVVFLQEV------I 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFLGKPKHCQY - - -
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                                                                                                                                                                                                                                                                                                                                  Similarity
                                                   -RIRQHLCTLGRSCNHDKEEGDAPSLAGFIWAGDLNVAERDYDRYFAGSYKAMQKC
                                                                                                                                                                                                                                                                                                                                                                         405 AA; 45193 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSQEIIP--
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel.
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                                                                                                                                                                                   -C-----AYLKKRAAS-YTIIT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1E9N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -TWDTKANNNLR--IPAAYKHRFDRIFFRAEEGHLIPQS
                                                                                                                                                                                                                                                                                                                                  5.2%; Score 101.5; 1
20.7%; Pred. No. 1.1;
                          NVFDAWEFLGKPKHCQYT-WDTKANNNLRIPAAYKHRFDRIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinetoplastida;
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21,
                                                                                                                                                                                                                                                                                                                   37; Mismatches
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Last
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                                                                                                                                                                                                                                                                                                                                                                      3BAFC1882DB8FCF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update)
annotation update)
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                                                                                                                                                                                                                                                                                                                    119;
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                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                   -GNEEG---
                                                                                                                                                                                                                                                                                                                                              405;
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RESULT 15
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         01-NOV-1999 (TrEMBLrel. 12, C:
01-NOV-1999 (TrEMBLrel. 12, L:
01-UN-2002 (TrEMBLrel. 21, L:
Hypothetical 57.7 kDa protein
SPBC9B6.1IC.
Schizosaccharomyces pombe (Fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q27811;

01-NOV-1996 (TrEMBLrel. 01, Created)

01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

01-MAR-2002 (TrEMBLR) (EC 3.6.1.3) (Fragment)
 Eukaryota;
                                                                                Q9Y7M8;
                                                                                           Q9Y7M8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tripneustes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tripneustes gratilla
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
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EMBL; U03978; AAA63592.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sea urchins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7673;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00018; EF_HAND; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                       AASYTIIT-----GNEEGY-----FTAILLKKGRVKFK----SQEIIPFPNTKMM
                                                                                                                                                                                                                                              TEIKLDPTCSVFITMNPGYAGRSDLPDNLKALFRTVAMMVPDYALISEIVLYSCGFIKAR
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1114 AA;
Fungi;
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                                                                                             PRELIMINARY;
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es pombe (Fission yeast).
Ascomycota; Schizosaccharomycetes;
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21.4%;
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                                 protein.
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                                            Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                       36; Mismatches
                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                 Score 101; DB Pred. No. 5.4;
                                                                                             PRT;
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Best Local Similarity 18.1
Matches 88; Conservative
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Hypothetical protein.
SD2 AA; 57650 MW; 54DFE2E7613B1A86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces. Schizosaccharomyces. NCBI_TaxID=4896;
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                                                               497 ANVQIV 502
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                                                                                                                                                                                                                                                                                                                                                                                                199 GKTHGIMIFWKSSLFK-KVQDLTIYYDDHDELPGRMNTKNIGCCVRLERVDDPSRGLFLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 FPHSGEALKWKNRSRMLANELTYYSPTLGCMQEVDAEFVPNFYKKLLGGLGYELHFIKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 RKPIAPPSNAPPEFNTDFIKREMLSIPNYAPFETEKSALDITIMTYNV--LAQTNIRRSM 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 DWQTQKALSAYFE-----LPENDQGWPRQPPTSFKSEAYVDLTNEDANDTTILEAS 112
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                                                                                                                                                                  EGHL--
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                                                                                                                                                                                                                                                                                                 IKCGGLPDNVFDAWEFL~GKPKHCQYTWDTKANNN------
                                                                                                                                                                                                                                                                                                                                                     TSHLESTREHSAERIRQ---LKTVLGKMQEAPDSTTVIFAGDTN------LRDQEV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----PSGTPLE------ 139
                                                                                                                                                                                                                                                                                                                                TTHLFWHPYGSYERLROGAILVKEVNKMAQSHPSWPVFIAGDENTEPFDTNFPALTTRPL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                 EEGYFTAILLKKGRVKFKSQEIIPF-----PNTKMMRNLLCV----NVSLGGNEFCLM 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----PERARGYCSCLALYSPDYVFLQEVIPPYCAYLKKR---AASYTI--ITGN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYRLSKLAISFFDQKKNKMADSIPVKKKGSAKGPP-SFVTPEYIEKQRQKKLEKMAKKAA 80
                                                                                                                                 QGHLDYIFVMNRDTSLQTPENQVVEGIKLKALLRVPLPSEMKEAEPLE-GRYPSDHVALM 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.1%; Score 100.5; DB 3; Length 502; 18.1%; Pred. No. 1.9; Indels 183;
                                                                                                                                                                                                                                -----LRIPAAYKHRFDRIFF----RAE 333
                                                                                                                                                              -IPQSLDLVGLEKLDCGRFPSDHWGLL 363
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: sp_archea:*
2: sp_bacteria
3: sp_fungl:*
4: sp_humanteb:
5: sp_nmammal:*
7: sp_mhc:*
8: sp_organel:
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_vertebr:
13: sp_virus:*
14: sp_urclass
15: sp_roterias:
16: sp_bacteria:
16: sp_bacteria:
17: sp_archeap
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
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sp_archeap:*
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sp_rvirus:*
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09XWG3
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Q8t214 dictyosteli
Q9y7m8 schizosacch
                                                                                                                                                                                                Q9jjx7 mus musculu
Q9d7n0 mus musculu
Q9xwg3 caenorhabdi
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Q9nuk5 homo
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29vgs4 drosophila
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                                                                                                                                                                                                                                                                             sapien
                                                                                                                                                                                                                                                             sapien
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Q9jmc1 rattus norv	Q9JMC1	11	1001	5.1	97.5	45
Q94648 plasmodium	Q94648	ഗ	3844		98	44
000362 homo sapien	000362	4	1275		98	43
	000360	4	1275	•	98	42
Q8sw87 encephalito	Q8SW87	տ	703		98	41
Q9bkp5 dictyosteli	Q9BKP5	տ	283		98.5	40
Q8xli6 clostridium	Q8XLI6	16	256		99.5	39
Q9un80 homo sapien	Q9UN80	4	1275	·	100	38
	000370	4	1275		100	37
O15463 homo sapien	015463	4	1261		100	36
Q91vf3 arabidopsis	Q9LVF3	10	458		100	35
Q8sd65 pseudomonas	Q8SD65	9	816		100.5	34
085672 clostridium	085672	2	695		100.5	$\frac{3}{3}$
homo	Q8TE30	4	1275		101	32
homo	015606	4	1275	5. 3	101	31
000378 homo sapien	000378	4	1275		101	30
homo	000368	4	1275		101	29
homo	Q12881	4	1275			28
homo	Q15604	4	1275		101	27
tryp	015921	J	405		101	26
000375 homo sapien	000375	4	1275		102	25
agr	Q8UEP1	16	265		102	24
homo	000366	4	1275		103	23
Q9y5k0 homo sapien	Q9Y5K0	4	1275		103	22
caeno	045711	ςī	288		103	21
listeria	Q8YA41	16	256		103.5	20
Q8yph2 anabaena sp	Q8YPH2	16	281	5. 5	104.5	19
022148 arabidopsis	022148	10	1374		105	18
Q8vcu0 mus musculu	Q8VCU0	11	667		105.5	17

ALIGNMENTS

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RESULT 1
095551
     Pype S., Declercq W., Ibrahimi A., Michiels C., vandenabeele P., van Rietschoten A.G.I., Dewulf N., de Boer M., Vandenabeele P., Huylebroeck D., Remacle J.E.; "TTRAP, a novel protein that associates with CD40, Tumor Necrosis Factor (TNF) Receptor-75 and TNF Receptor-Associated Factors (TRAFs), and that inhibits Nuclear Factor-kappaB activation."; J. Biol. Chem. 275:18586-18593(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY 1999 (TrEMBLrel. 10, Created)
01-MAY 1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DJ30M3.3 (TRAF and TWF receptor associated protein)
protein 2) (Hypothetical 40.9 KDa protein).
DJ30M3.3 OR TTRAP OR EAP2.
Strausberg R.;
Submitted (NOV-2001) to the
EMBL; AL031775; CAA21141.1;
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=20309820; PubMed=10764746;
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                                                                                      Submitted (NOV-1999) to the
                                                                                                 Li R., Pei H.,
"EAP2, a Novel
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    Submitted (JAN-1999)
                                             TISSUE-SKIN;
                                                           SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                 Papas T.S.;
Protein Interacting with ETS1.";
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Primates;
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    EMBL/GenBank/DDBJ databases
                                                                                      EMBL/GenBank/DDBJ databases
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Q91sq7 Q9s219 Q8unx2 Q9cmw2

pasteurella mus musculu

Q92x70

rhizobium m arabidopsis human immun streptomyce

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RESULT
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Best Local Similarity
Matches 362; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9NYY9 PRELIMINARY;
Q9NYY9;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
AD022 protein.
                                                                                                                                                                   TISSUE-ADRENAL GLAND;
Song H., Gao G., Peng Y., Ren S., Chen Z., Han Z.;
Song H., Gao G., Peng Y., Ren S., Chen Z., Han Z.;
"A novel gene expressed in human adrenal gland.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF223469; AAF64144.1;
InterPro: ITR005135; Exo_endo_phos.
Pfam; PF03372; Exo_endo_phos; 1.
SEQUENCE 362 AA; 40956 MW; D6D607DE521C27E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AD022
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EMBL; AF201687; AAG35600.1; ..
EMBL; BC017553; AAH17553.1; ..
InterPro; IPR005135; Exo_endo_phos.
Pfam; PF03377; Exo_endo_phos; 1.
Receptor; Hypothetical protein.
SEQUENCE 362 AA; 40929 MW; 37892E125DB64410
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361
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                                                                                        Conservative
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Last sequence update)
Last annotation updat
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                                                                                   Score 1897; DB 4;
Pred. No. 5.3e-150;
0; Mismatches 1;
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Pred. No. 2e-150;
; Mismatches 0;
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01-JUN-2002 (TrEMBLrel. 21, Last annotation
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                                                                                                                                                    YFEPPVEESALERRPETISEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWN 120
AIMLKKSRVKLKSQEIIPFPSTKMMRNLLCVHVNVSGNELCLMTSHLESTRGHAAERMNQ
                  AIMLKKSRVKLKSQEIIPFPSTKMMRNLLCVHVNVSGNELCLMTSHLESTRGHAAERMNQ
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AA; 40869 MW;
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative TRAF and TNF receptor associated protein.
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J. Biol. Chem. 275:18586-18593(2000).
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Pype S. Declercq W., Ibrahimi A.,
Van Rietschoten A.G.I., Dewulf N.,
Huylebroeck D., Remacle J.E.;
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Mammalia; Eutheria;
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MGI:1860486; Ttrap.
rPro; IPR005135; Exo_endo_phos.
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HRFDRIFFR--AEEGHLIPQSLDLVGLEKLDCGRFPSDHWGLLCTLNVVL
                                                                                                                                    PESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWDTQMNSNLGITAAC 311
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Rodentia;
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68.4%;
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Pred. No. 1e
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de Boer N
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RESULT 5
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RA Alzawa K., Izawa M., Nishi K., Riyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Riyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Matsuda H.A., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rojuez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                    09xWG3;
01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
Y63D3A.4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9D7NO;
Q1-UUN-2001 (TrEMBLrel. 17, Created)
Q1-UUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-UUN-2002 (TrEMBLrel. 21, Last annotation updat
Traf and Tnf receptor associated protein.
           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Koncsuki s
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                            Q9XWG3
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 NCBI_TaxID=6239;
                                                                        Y63D3A.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF03372; Exo_
SEQUENCE 157 AA;
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                                                                                                                                                                                                                                                                    MMRNLLCVHVNVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQEAPESATVIFAGDT
                                                                                                                                                                                                                                                                                                                                                             NLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWDTQMNSNLGITAACKLRFDRIFFRAA 323
                                                                                                                                                                                                                                                                                                       AEEGHIIPRSLDLLGLEKLDCGRFPSDHWGLLCNLDIIL 362
                                                                                                                                                                                                                                                                                                                                           NLRDQEVIKCGGLPDNVFDAWEFLGKPKHCQYTWDTKANNNLRIPAAYKHRFDRIFFR--
                                                                                                                                                                                                                                                                                                                                                                                                                  MMRNLLCVNVSLGGNEFCLMTSHLESTREHSAERIRQLKTVLGKMQEAPDSTTVIFAGDT
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                                                                                                                                                                               PRELIMINARY;
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AA; 17876 MW;
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77.4%;
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12,
21,
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Last annotation update)
                                                                                                                                            Created)
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i J., Fukuda S.,
S., Yamanaka I.,
                                     Rhabditoidea;
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Best Loc
Matches
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Q1-MAY-2000 (TrEMBLrel. 13, C
Q1-MAY-2000 (TrEMBLrel. 13, L
Q1-JUN-2002 (TrEMBLrel. 21, L
F25C2O.3 protein.
F25C2O.3.
                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Aggnoliophyta; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBL_TaxID=3702;
[1]
SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Li
Li J., Lee J.M., Kremenetskaia I., Luros J., Ngan I., Liu A.,
Gonzalez A., Altafi H., Araujo R., Chao Q., Conn L., Conway A.
Dunn P., Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shi
Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis
"Arabidopsis thaliana chromosome 1 BAC F35C20 sequence.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF03372; Exo_endo_phos; 1.
SEQUENCE 362 AA; 40893 MW; 7895C47504866E52
                                                                                                                                                                                                                                                                                  Q9SA95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            investigating biology.";
Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                   348
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08; Conservative
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Pred. No. 7.1e-27;
5; Mismatches 142
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                                         Conway A.B.
ey D., Shinn
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29 VGS4
20 VGGS4
20 VGGS
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An Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
An Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
An Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
An George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
An Edendon R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
An Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
An Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
An Barandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
An Ballew R.M., Basu A., Baxendale J., Bayakataroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
An Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
An Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
An Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
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CG4796.
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InterPro;
InterPro;
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  Durbin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Pterygota; Neoptera; Endopterygota; Diptera Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9VGS4;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9VGS4
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EMBL; ACO
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                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAEEGHIIPRSLDLLG-LEKLDCGRFPSDHWGLLCNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLPDKWVDVWEVL-KPGDLGFTYDTKANPMLSGNRALQKRLDRILCRLDDYKLGGIEMVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLESPCPGPPKWDQMFSRERVEQAKEAIEILR---PNANVIFGGDMNWCD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLES----TRGHAAERMNQLKMVLKKMQEAPESATVIFAGDTNLRDREVTRCGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILSYNVWFREDLELN----LRMRAIGHLIQLHSPHLICFQEVTPEIYDIFRKSNWWKAYSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LPNNIVDVWEFLGKPKHCQYTWDTQMNSNLGITAACKLRFDRIFFR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVSVDVAVSRGYYCMLL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NYETITGHEEGYFTAIMLKKSRVKLKSQETIPFPSTKMMRNLLCVHVNVSGNE-LCLMTS
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Pro; IPR001969; Aspprotease_site.
Pro; IPR005135; Exo_endo_phos.
K., Doup L.E., Downes M.,
K.J., Evangelista C.C., F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein.
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PS01358; ZF_RANBP2_1; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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30.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation updat
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fly)
  Ferraz C.,
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5.3e-11;
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  Ferriera
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  Fleischmann
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RESULT Q872L4
ID Q8 AC Q8 DT 0:
DT 0:
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DT 0:
OT 0
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeqwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McLson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syliskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Schos R.A., Myers E.W., Rubin G.M., Venter J.,
RM AFON369, Aarstafin 1. -

DR EMBL, AFON369, Aarstafin 1. -

DR EMBL, AFON369, Aarstafin 1. -
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Best Loc
Matches
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 41.3 kDa protein.
Dictyostellum discoideum (Slime mold).
Eukaryota, Mycetozoa; Dictyostellida; Dictyostellum
NCBI_TaxID-44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE003690; AAF54601.1; -. FlyBase; FBgn0037872; CG4796. InterPro; IPR005135; Exc_endo_phos.
                                                                                                                                                                                                                                    Q8T2L4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WGLLCNLDII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---VTRCGGL-----PNNIVDVWEFLGK----PKHCQYTWDTQMNSNLGIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LADEDVADGLRCLKLNSVSRVCSAPVE-----GDDIRLLQWNILSQTLGQHNDGFVRCP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTNEETTD-----STTSKI--SPSEDTQQENGSMFSLITWNI-------DGL---- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----IREEGEECHTIDYVFYTPDRLKIKNCLDFPAGEQIGKNRTPSFQYPSDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCDLLRLGSAYADVKLDREEILHPN--ADVGEFVAKSMKREPPYT--TWK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFCVATTHLKARHGALLAKLRNEQGRDLIRFVKQFAGDTPLLLCGDFNAEPVEPIYATIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELCLMTSHLESTRGH---AAERMNQLKMVLKKMQEAPESATVIFAGDTNLRDRE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEALTWEHRKYLIVQEILQNQPDVICLQEV--DHFKFLQTVLGSQNY-----AGIFFP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -DLNNLSERARGYCSYLALYSPDVIFLQEVIPPYYSYLKK--RSSNYEIITGHEEGYF-- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACKLRFDRIFFRAAAEEGHII----PRSLDL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF03372; Exo_endo_phos; 1
NCE 449 AA; 50275 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TAIMLKKSRVKLKSQEIIPFPSTKMMRNLLCV----HVNVSGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 127.5; DB 5; Length Pred. No. 0.023; Mismatches 108; Indels
                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1607DF25A418A024 CRC64;
                                                                                                                                                                                                                                                                   361
                                                                                                                                                                                                                                                                   ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LGLEKLDCGRFPSDH
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Best Local S
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Best Loc
Matches
                                                                                                                     Matches
                                                                                                                                                                                                 STRAIN-972H-; Wood V., Rajandream M.A., Barrell B.G., Volckaert G.; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases EMBL; AL049769; CAB42372.1; -InterPro; IPR005135; Exo_endo_phos. Pfam; PF03372; Exo_endo_phos; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  Q9Y7M8 PRELIMINARY; PRT; 502 AA. Q9Y7M8; 01-NOY-1999 (TrEMBLrel. 12, Created) 01-NOY-1999 (TrEMBLrel. 12, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical 57.7 kDa protein. SPBC986.11C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P. Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noege "Sequence and Analysis of Chromosome 2 of Dictyostelium."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                          Hypothetical SEQUENCE 5(
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
STRAIN=AX4;
                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein. SEQUENCE 361 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AC115596; AAL92312.1; -.
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGGREAAEEEGEPEVKKRRLLCVEFASVASCDAAVAQCFLAENDWEMERALNSYFEPPVE 67
RKPIAPPSNAPPEFNTDFIKREMLSIPNYAPFETEKSALDITIMTYNV--LAQTNIRRSM 138
                                                                                     RG-----LQRLDYRIKEWDVDFQAYLEKLNATKPIIWCGDLNVAHTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K----SVLSKGFTEYVEKENPDVLCLQETKINP--SNIKKDQMPKGYEYHFIEADQKGHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLNNLSERARGYCSYLALYSPDYIFLQEV-IPPYYSYLKK----RSSNYEIITGHEEGYF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAAAKKKSK--DEDEDEEEKEEEEETNKTTASVSIAIDNLDEPKVEENQMKIISWNVAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESALERRPETISEPKTYVDLTNEETTDSTTSKISPSEDTQQE---NGSMFSLITWNIDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEEKEEVEEE-EEEDKKRKLVKKTPAKKA--
                          --- ISPSEDTQQENGSMF--
                                                        DYRLSKLAISFEDQKKNKMADSIPVKKKGSAKGPPSFVTPE-YIEKQRQKKLEKMAKKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -TAIMLKKSRVKLKSQEIIPFPSTKMMRNLLCVH-----VNVSGNELCLMTSHLES--T
                                                                                                                   90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
60; Conserv
                                                                                                                                Similarity
                                                                                                                                                                            al protein.
502 AA; 57650 MW; 54DFE2E7613B1A86 CRC64;
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                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.4%;
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                                                                                                                                5.9%;
18.2%;
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                                                                                                                   65;
                                                                                                                                Score 113;
Pred. No. 0.
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                                                                                                                   Mismatches
                                                                                                                                 DB 3;
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                                                                                                                   142;
                            --SLITWNIDGLDLNNL----
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                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                     198;
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                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                      RB0092 OR SMB20092.
Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid BSymB (megaplasmid 2).
Bacteria; Proteobacteria; alpha subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          092X70:
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
Hypothetical protein RB0092
                                                                                                                                                                                          Pfam; PF03372; Exo_endo_phos; 1.
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 252 AA; 27376 MW; A8B6F28C8A8316AE CRC64;
                                                                                                                                                                                                                                                                                                MEDLINE=21396508; PubMed=11481431;
Finan T.M., Weidner S., Wong K., Buhrmester
Vorhoelter F.J., Hernandez-Lucas I., Becker
Golding B., Puehler A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q92X70
                                                                                                                                                                                                                                                          "The complete sequence of the 1,683-kb pSymB megaplasmid fixing endosymbiont Sinorhizobium meliloti."; proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139
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                                                                                                                                                                                                                                 EMBL; AL603642; CAC48492.1; -.
InterPro; IPR005135; Exo_endo_phos.
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                               94
 244 VLKK---MQEAPESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLG-KPKHCQYTWDT
                                                                                                                                     Local Similarity
es 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRCGGLPNNIVDVWEFLGKPKHCQYTW-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FPHSGEALKWKNRSRMLANELTYYSPTLGCMQEVDAEFVPNFYKKL-LGGLGYELHFIKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YPSDHVALMANVQIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FPSDHWGLLCNLDII 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFTNWAHAYQGHLDYIFVMNRDTSLQTPENQVVEGIKLKALLRVPLPSEMKEAEPLE-GR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPESTASTPKKRILHVQNDYVPHYRSFYQQHEQNPVLFSLYSVGYKLVHPENAKNTFDHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt TTHLFWHPYGSYERLRQGAILVKEVNKMAQSHPSWPVFIAGDFNTEPFDTNFPALTTRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGKTHGIMIFWKSSLFKKVQDLTIYYDDHDELPGRMNTKNIGCCVRLERVDDPSRGLFLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGYFTAIML-KKSRVKLKSQEIIPF-----PSTKMMRNLLCV----HVNVSGNELCLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FFR--AAAEEGHI--
                            ---TALPMRLIKAAPLPSSSEPRGALWVEIDVAAVKLQVIVTHL-GLRG--AERLRQATA
                                                                                {\tt IAAVIAECQPDVIALQEVDVGRARTGGIDQAHMIATHLNMEAEFHPALHLEDEKYGDAVL
                                                                                                          VCSYLALYSPDVIFLQEV------IPPYYSYLKKRSSNYEIITGHEEGYFTAIM 183
                                                     LKKSRVKLKSQEIIPFPSTKMMRNILLCVHVNVSGNELCLMTSHLESTRGHAAERMNQLKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---SERARGYCSYLALYSPDVIFLQEV----IPPYYSYLKKRSSNYEIITGHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            Sinorhizobium
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                                                                                                                                                     5.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                  Score 111.5; D
Pred. No. 0.22;
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                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         subdivision; Rhizobiaceae
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                                                                                                                                                                 DB 16;
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Cowie
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                                                                                                                                         57;
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Q9LSQ7
                                                                                                RESULT 13
Q9S2L9
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Best Local
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Genomic DNA, Chromosome 5, BAC clone:F24B18.
Arabidopsis thailana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY 2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein SCO2125.
SCO2125 OR SC6E10.19C.
                                                                      Q9S2L9
Q9S2L9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structural analysis of Arabidopsis thaliana chromosome Submitted (APR-1999) to the EMBL/GenBank/DbBJ databases. EMBL; AB026634; BAA97521.1; SEQUENCE 720 AA; 81852 MW; 65B822BCF991672C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaneko T., Katoh T.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                                              CDAAVAQCFLAENDWEMERALNSYFEPPVEESALERRPETISEPKTYVDLTNEETTDSTT
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                                                                                                                                                                                                                                                                                     PPYYSYLKKRSSNYEIITGHEEGYFTAIMLKKSRVKLKSQEIIPFPSTKMMRNLLC----
                                                                                                                                                                                                                                                                                                                                                                                                                          DGFREIREREGIPDLEPESDYNSLIRKNKKKKKKKKKKKKKKNVRESSSVASEIDKRDVEANT
                                                                                                                                                                                                                                                                                                                                                                                                                                           VIFAGDTNLRDREVT-RCGGLPNNIVDVWEFLGKPKHCQY 295
                                                                                                                                                                                                           KLHAEVTAEEKLRVAYEKAYKILNNLDQNGAESSELYEAETL--VKLHLSKVNVSVRAVE
                                                                                                                                                                                                                                                             --YHQPLGSQFKGFASRVIGSSGTTTRDLVLKRRFRLDDLAV----SLSMTLEKLYMWEK 410
                                                                                                                                                                                                                                     -VHVNVSGNELC----
                                                                                                                                                                                                                                                                                                                   SDEEVSDEAYESSSCFSESSGS--GLTDLRKVVERINSICGKAAGNSEVSELLEVSRVV 356
                                                                                                                                                                                                                                                                                                                                           SKISPSEDTQQENGSMFSLITWNIDGL-DLNNLSERARGVCSYLALYS--PDVIFLQEVI 154
                                                                                                                                                      SISMRIHKIRDEELSFQVIEIINGFKTMWRFLAKCHHKQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
78; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 108.5;
Pred. No. 1.7;
                                                                                                                                                                                                                                      -LMTSHLESTRGHAAERMNQLKMVLKKMQEAPESAT
                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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RESULT 14
Q8UNX2
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AC Q8UNX
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Matches 56
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.B., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Redenbach M., Kieser H.M., Johnson R. Redenbach M., Kieser H.M., Lower R. Redenbach M., Hopwood D.A.; Kinashi H., Hopwood D.A.; "A set of ordered cosmids and a detailed genetic and physical map the 8 Mb Streptomyces coelicobor A3(2) chromosome."; Mc1 Microbiol. 21:77-96(1996).
 Q8UNX2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hopwood D.A.;
"Complete genome sequence of the coelicolor A3(2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 417:141-147(2002).

EMBL; AL109661; CAB51973.1; -.

InterPro; IPR005135; Exo_endo_phos.

Pfam; PF03372; Exo_endo_phos; 1.

Hypothetical protein.

SEQUENCE 253 AA; 26691 MW; 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97000351; PubMed-8843436; Redenbach M., Kieser H.M., Denapaite D.,
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SEQUENCE FROM N.A.
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                                                                                                                      GHIIPRSLDLLGLEKLDCG-
                                                                                                                                                                                DREVTRCGGLPNNIVDVWEFLGKPKHCQYTWDTQMNSNLGITAACKLRFDRIFFRAAAEE
                                                                                                                                                                                                                AAAVVRIGGARIGVLSSHLSL---DADERHEQAGLLLDHL-AALGVKHAVAGGDLNERPG
                                                                                                                                                                                                                                                                                                                                                                  STTSKISPSEDTQQENGSMFSLITWNIDGLDLNNLSERARGVCSYLALYSPDVIFLQEVI 154
                                                                                                                                                                                                                                            LCVHVNVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQEAPESATVIFAGDTNLR--
                                                                                                                                                                                                                                                                                                      PPYYSYLKK-----RSSNYEIITGHEEGYFTAIMLK-KSRVKLKSQEIIPFPSTKMMRNL
                                                                                                                                                                                                                                                                                                                                    ATSLPALPNSRTEPDGSAVIRVLSYNI ---- RSLRDDTDALARVIKACAPDLVLLQEA- 55
                                                                                                                                                                                                                                                                        PRFFRWRKKITRLAAAGDLVLLSGGGTAAGPALLCSLRATVERTEDVLLPLTPGRHRRGI 115
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                PRELIMINARY;
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                                                                                         GIEVLGCGVPSGLAGVAEDDLRAATDHLPVLTALRV
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                                                                                                                                                                                                                                                                                                                                                                                                              5.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J., Barrell B.G., Rajandream M.A.; to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 108; DB Pred. No. 0.44;
                PRT;
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RESULT 15
Q9CMW2
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Best Local
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01-JUN-2001 (TrEMBLrel. 17, L
01-JUN-2002 (TrEMBLrel. 21, L
Hypothetical protein PM0691.
PM0691.
                                                                                                                                                                                Q9CMW2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang P.F., Bouma P., Park E.J., Margolick J.B., Robinson J.E., Zolla-Pazner S., Flora M.N., Quinnan G.V. Jr., "A variable region 3 (V3) mutation determines a global neutralization phenotype and CD4-independent infectivity of a human immunodeficiency virus type 1 envelope associated with a broadly cross-reactive, primary virus neutralizing antibody response.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; Retroid
NCBI_TaxID=11676;
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InterPro; IPR000777; GP120.
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EMBL; AF443202; AAL66251.1;
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MEDLINE=21145866; PubMed=11248100;
May B.J., Zhang Q., Li L.L., Paust
                         STRAIN=PM70;
                                      SEQUENCE FROM N.A.
                                                                NCBI_TaxID=747;
                                                                           Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Pasteurella.__
                                                                                                      Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                     CKNVSTVQCTHGIRPVVSTQLLLNGS---LAEEEVV-IRSENFTNNAKTIIVHLNESVQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                -KRSSNYEIITGHEEGYFTAIMLKKSRVKLKSQEIIPFPSTKMMRN--LLCVHVNVSGNE
                                                                                                                                                                                                                                                                                                                                         ATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    863 AA;
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Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL; AE006105; AAK02775.1; -.
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Dupressoir A., Barbot W., Loireau M.P., Heidmann T.;
Dupressoir T.;
"Characterization of a mammalian gene related to the yeast CCR4
general transcription factor and revealed by transposon insertion.";
J. Biol. Chem. 274:31068-31075(1999).
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"Characterization of two age-induced intracisternal A-particle-related transcripts in the mouse liver. Transcriptional read-through into an open reading frame with similarities to the yeast ccr4 transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and circadian regulation."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                          entities requires a license agreement (S
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
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by non-profit institutions as long
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                                                AF183960; AAD56547.1; -. AF199491; AAG01384.1; -. U70139; AAB62717.1; ALT_
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Rodentia;
  Exo_endo_phos
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Biological rhythms.
COMPLICT 123 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nocturnin (CCR4 protein homolog). CCRN4L OR NOC OR CCR4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOCT_HUMAN STANDARD; PRT; (9UK39; 09HD93; 09HD94; 09HD95; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence up 15-JUN-2002 (Rel. 41, Last annotation 15-JUN-2002 (Rel. 
                                                                                                                                  and circadian regulation";

Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: COMPONENT OF THE CIRCADIAN CLOCK OR DOWNSTREAM EFFECTOR OF CLOCK FUNCTION. EXHIBITS A HIGH AMPLITUDE CIRCADIAN RHYTHM WITH MAXIMAL LEVELS IN EARLY EVENING. IN CONSTANT DARKNESS OR CONSTANT LIGHT, THE AMPLITUDE OF THE RHYTHM DECREASES (BY SIMILARITY).

-i- SIMILARITY: BELONGS TO THE CCR4/NOCTURIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                        This
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"Mammalian homologs of Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 67-431 FROM
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                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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SPRAIN=Rd / KW20 / AFCC 51907;

SPRAIN=Rd / KW20 / AFCC 51907;

MEDLINE-95350630; PubMed-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirk Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Mer McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
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01-NOY-1995 (Rel. 32, Last sequence upolity)
15-JUN-2002 (Rel. 41, Last annotation upolity)
Exodoxyribonuclease III (EC 3.1.11.2)
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EMBL; AF199493; AAG01388.1; --
EMBL; AF199494; AAG01389.1; --
Genew; HGNC.14254; CCRN4L.
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Pred. No. 0.0036;
6; Mismatches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                               subdivision;
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> A (IN REF. 2).
> T (IN REF. 2; AAGO138
> T (IN REF. 2).
61EF484E8D29AF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                             update
                                                                                                                                                                                                                                                                                                                                                                                                                               267
                                                                                                                                                                                                                                                                                                                                   update)
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                                                            Clayton R.A., Kirkness
Dougherty B.A., Merrick
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                                                                                                                                                                                                                                               Pasteurellaceae;
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RESULT 5
PHL_LEPIN
ID PHL_L
AC P1762
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Best Local :
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SEQUENCE
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGREAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Nuclease;
METAL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR; HI0041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Whole-genome random sequencing Rd."; Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                                                     124 ISFITWNIDGLDGCNLPERARGVCSCLALYSPDVVFLQE--VIPPYCAYLKKRAASYTII
                                                                                                                                                                                                                                                     56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              erpro; IPR000097; APendonclsel.
erpro; IPR004442; ExoDNase_III.
erpro; IPR004808; ExoIII_xth.
erpro; IPR004515; Exo_endo_phos.
m; PF03372; Exo_endo_phos; I.
RFAMS; TIGR00195; exoDNase_III; 1.
RFAMS; TIGR00633; xth; 1.
RFAMS; TIGR00633; xth; 1.
SITE; PS00726; AP_NUCLEASE_F1_2; 1
SITE; PS00727; AP_NUCLEASE_F1_3; 1
SITE; PS00728; AP_NUCLEASE_F1_3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           progressively in phosphates.
SUBUNIT: MONOMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: Degradation of double-stranded DNA. It is progressively in a 3'-to 5'-direction, releasing nucleoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REMOVES THE 3'S
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                                                                                                                                                                                          QGESRAHETKFPAKEKFYADLQQYLEK--EHDKSNPILIMGDMNISPSDLDIGIGDENRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY)
                                                                                                                                     RWLRTGKCSFLPEERAWYQRLYDYGLEDSFRKLNPTANDKFSWFDYRSKGFDDNRGLRI-
                                                                                                                                                                                                                                                  HHGQKGHYGVALLTKQEPKV-IRRGFPTDNEDAQKRIIMADLE---TEFGLLTVINGYFP
                                                                                                                                                                                                                                                                              TGNEEGYFTAILLKKGRVKFKSQEIIPFPNTKMMRNLLCVNVSLGGNEFCLMT---
                                                                                                                                                                                                                                                                                                          MKFISFNINGLRA-----RPHQLEAIIEKYQPDVIGLQEIKVADEAFPYEITENLGYHVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U32689;
                                                                                                                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                      ·SHLESTREHSAERI-RQLKTVLGKMQEAPDSTTVIFAGDTNLRDQEVI---
                                                                                                                                                                                                                                                                                                                                                                                                                         34
259
267 AA;
                                                                                                                                                                  -KCGGLPD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S THE DAMAGED
                                                                               -DHILVSQKLAERCVDVGIALDIRAMEK---
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ilarity 22.2%;
Conservative 4
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MAGED DNA AT CYTOSINES AND GUANINES BY CLEAVING
THE AP SITE BY A BETA-ELIMINATION REACTION
                                                                                                                                                                                                                                                                                                                                                                                                                           31025
                                                                                                -AEEGHLIPQSLDLVGLEKLDCGRFPSDH
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                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0.08
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  ease; DNA repair; Complete proteome MAGNESIUM OR MANGANESE (BY SIMILAR: GENERAL BASE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                            Score
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No. 0.
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PHL_LEPIN P17627;

PRT;

556

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RESULT 6
PR31_YEAST
ID PR31_YEAST STAN
AC P49704;
DT 01-OCT-1996 (Rel. 3
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-i- CATALYTIC ACTIVITY: Sphingomyelin + H(2)0 = N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
sphingomyelinase C precursor (EC 3.1.4.12) (Sphingomyelin phosphodiesterase) (SMASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leptospira interrogans.
Bacteria; Spirochaetales; Leptospiraceae; Leptospira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Serovar Hardjo / isolate Sponselee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X52176; CAA36424.1; -. PIR; S22634; S22634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      choline phosphate.
                                                                                                                                                                        YHQMLCILNVNNP----KYVGVP----FTWDTKTN----EIAAFYYKKVE--
                                                                                                                                                                                                                                                                                              TLGLYRTDAFTNGGVVIVSKWPIEEKIQHVFKEKGCGADVFSN----KGFAYVRIDKNGR
                                                                                                                                                                                                                                                                                                                                                           IVSSNYIQNQDVIVFDEAFDTDARKILLDGVRSEYPY-----QTDVIGRTKKGWDA
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                                                                                                                                           IPQSLDLVGLEK 349
                                                                                                                                                                                                    QEVIKCGGLPDNVFDAWEFLGKPKHCQYTWDTKANNNLRIPAAYKHRFDRIFFRAEEGHL
                                                                                                                                                                                                                                   KFHIIGTHVQAQDSGCANLGVVSRVNQFNEIRDFIDSKKIPKNEMVLIAGDLNVIKGSRE
                                                                                                                                                                                                                                                                 EFCLMTSHLESTREHSA-----ERIRQLKTVLG--KMQEAPDSTTVIFAGDTNL----RD
                                                                                                                                                                                                                                                                                                                                                                                                                      DLTGSGSVSSSPADAAPENSILANSIPENMGIKILTHNVFLLPKTLPGWGNWGQNERAQR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pro; IPR005135; Exo_endo_phos.
PF03372; Exo_endo_phos; 1.
                                                                                                            -PAYLDYIFVSK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal
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556 AA;
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                                                                                                                                                                                                                                                                                                                              -FT---AILLKKGRVKFKSQEIIP-----FPNTKMMRNLLCVNVSLGGN
                                 STANDARD;
   34,
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63268 MW;
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    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 99.5;
Pred. No. 0.
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                                   494
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Best Local S
Matches 80
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EMBL; Z72876; CAA$77094.1; -.
SGD; S0003323; PRP31.
Interpro; IPR002687; Nop.
Pfam; PF01798; Nop; 1.
ProDom; PD004104; Nop; 1.
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16-OCT-2001 (Rel. 4
Pre-mRNA splicing 1
PRP31 OR YGR091W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weidenhammer E.M., Singh M., Ruiz-Noriega M., "The PRP31 gene encodes a novel protein requisisplicing in Saccharomyces cerevisiae."; Nucleic Acids Res. 24:1164-1170(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wedler H., Scharfe M.,
Submitted (MAY-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96184869; Weidenhammer E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA processing; mRNA splicing; Nuclear protein.
CONFLICT 361 394 TNPKRKELGENLGSTRKNSDYRMSDNYKIGWNLA
 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: REQUIRED FOR PRE-MRNA SPLICING
                                                                                                                                                                                                                                                                                                              TQILEAN---SILEN-----LWKLQ-----EDIGQYIASKISIIAPNVCFL--VGP
                                                                                                                                                                                                                                                                                                                                                                         VISILENENYSKNESDELFFHL-ENKAKLTREQILVLTMSMKTSFKNKEPLDIKTR----
NQQADEFLISLGHNTEQPNLSPEMVQMHK 477
                              FFRAEE----GHLIPQ---SLDLVGLEK 349
                                                                                          EFLGKPKHCQYTWDT----
                                                                                                                                                                                                                  KFKSQEIIPFPNT--KMMRNLLCVNVSLGGNEFCLMTSHLESTREHSAERIRQLKTVLG-
                                                                                                                                                                                                                                                                               PYCAYLKKRAAS----
                                                                                                                                                                                                                                                                                                                                              TTILEASPSGTPLEDSSTISFITWNIDGLDGCNLPERARGVCSCLALYSPDVVFLQEVIP
                                                           NL---AKQEQTVLDSYGEEVGLGMSNTSLQQAVGATSGSRRSAGNQAKLTKVMKHRISEA
                                                                                                                         KWKAELSKKARKLSEAPSISETKALPIPETNPKRKELGENLGSTRKNSDYRMSDNYKIGW
                                                                                                                                                                                      -FASDMIQKFPVSVHKQMLRMLCAKVSL----
                                                                                                                                                                                                                                                EIAAQLIAHAGGVLEFSRIPSCNIASIGKNKHLSHELHTLESGVRQEGYL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   494
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                      ----KMQEAP--DSTTVIFAGDTNLRDQEVIKCGG------LPDNVFDAW
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40, Last annotation update)
factor PRP31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 98; DB 1;
Pred. No. 0.69;
9; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REF. 2).
1C320B8630EEF5C8 CRC64;
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required for pre-mRl
                                                                                                                                                                                      ----AARVDAGQKNGDRNTVLAH
                                                                                                                                                                                                                                                                                                                                                                                                                                        116;
                                                                                             -KANNNLRIPAAYKHRFDRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 494;
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A2MG_MOUSE
                       SIGNAL
CHAIN
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    de Strooper B., van Leuven F., van den Berghe H.;
"Molecular cloning of the mouse gene coding for alpha 2-macroglobuli
and targeting of the gene in embryonic stem cells.";
Genomics 22:519-529(1994).
-i- FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY
UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH,
CALLED THE 'BAIT REGION' WHICH CONTAINS SPECIFIC CLEAVAGE SITES
CALLED THE 'BAIT REGION' WHICH CONTAINS SPECIFIC CLEAVAGE SITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       macroglobulin, deduced from protein subunits and from molecular cloning Eur. J. Biochem. 210:319-327(1992).
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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                                                                                                                                                                                  MGD; MGI:87854; A2m.
InterPro; IPR002890; A2M_N.
InterPro; IPR001599; MacrogloblnA2
                                                                                                                                                                                                                                                                                                                                                                 or send an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alpha-2-macroglobulin
                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95095249; PubMed=7528166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-161 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT REGION, A COMFORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH TRAPS THE PROTEINASE. THE ENTRAPED ENZYME REMAINS ACTIVE WHICH THAP MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR WEIGHT SUBSTRATES (BREATLY REDUCED). FOLLOWING CLEAVAGE IN THE BAIT REGION A THIOLESTER BOND IS HYDROLYZED AND MEDIATES THE COVALENT BINDING OF THE PROTEIN TO THE PROTEINASE.

TISSUE SPECIFICITY: PLASMA.

DEVELOPMENTAL STAGE: CONTRARY TO THE RAT PROTEIN, WHICH IS AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          den Berghe H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IN CIRCULATION.
SIMILARITY: TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leuven F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENTAL STAGE: CONTRARY TO THE RAT PROTEIN, WHICH ACCUTE PHASE PROTEIN, THIS PROTEIN IS ALWAYS PRESENT AT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                       U06977;
P01023;
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                                                                                                                                                PF00207; A2M; 1.
PF01835; A2M_N; 1.
                                                                                            protease
                                                                                                                                                                                                                                                                                                                                                                 requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                         PS00477;
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1240
686
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AAA87890.1; -.
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                                                                                               inhibitor;
24
1239
1495
744
                                                                                                                    ALPHA_2_MACROGLOBULIN;
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                                                           Glycoprotein; Plasma; Bait region; Signal. POTENTIAL.
                  ALPHA-2-MACROGLOBULIN 165 KDA SUBUNIT ALPHA-2-MACROGLOBULIN 35 KDA SUBUNIT.
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of the cDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALPHA-MACROGLOBULIN FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
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Best Local
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Q55445;
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      Sugiura M., Tabata S.; "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
                              SEQUENCE FROM N.A.
MEDLINE-96127529; PubMed-8590279;
MEDLINE-96127529; Sato S., Ko
                                                                                                         16-0CT 2001 (Rel. 40, Created)
16-0CT 2001 (Rel. 40, Last ser
16-0CT 2001 (Rel. 40, Last and
Hypothetical methyl-accepting
                                                                                                                                                                                                      1355 DGKAPFALQVNTLPLNFDKAEDHRTFQIRINVSYTG---ERPSSNMVI
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CONFLICT
                                                                                        Synechocystis sp.
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                                                                       NCBI_TaxID=1148;
                                                                                  Bacteria;
                                                                                                    SLL0041.
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the Euro
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SMART; SM00065; GAF; 2.
SMART; SM00304; HAMP; 1.
SMART; SM00283; MA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence analysis of the genome of the unicellular cyanobacterium synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.", DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura 1 Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Mosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumu Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001090; Me_chemotaxis InterPro; IPR001294; Phytochrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSORY TRANSDUCERS FAMILY -1- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
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HSHRNLDQPLAVAGDELAIADQTIDALSAQVEKL
                            YKHR-FDR-IFFRAEEGHLIPQSLDLVG--LEKL
                                                                          STTVIFAGDTNLRDQEVIKCGGLPDNV---FDAWEFLGKPKHCQYTWDTKANNNLRIPAA
                                                            STT-----KQIRDQILI--GLLVTAVGAAFVAYWMVGE:
                                                                                                                                                   QEIIPFPNTKMMRNLLCVNVSLGGNEFCLMTSHLESTREHSAERIRQLKTVLGKMQEAPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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PS50046; PHTTOCHROME_2; 2.
Cical protein; Transducer; Complete proteome.
Cical protein; To8334 MW; 58C5A765E1275FDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2:153-166(1995).
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IPR003018; GAF.
IPR003660; HAMP.
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Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HELICASE; HAS ATPASE ACTIVITY.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: BELONGS TO THE HELICASE FAMILY. SKI2 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rowen L.,
Banta A.,
                                                                                                                                                                                                                  modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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Dangel A.W., Shen L., Mendoza A.R., Wu L.-C., Yu C.Y.;
Dangel A.W., Shen E., Mendoza A.R., Wu L.-C., Yu C.Y.;
"Human helicase gene SKIZW in the HLA class III region exhibi
striking structural similarities to the yeast antiviral gene
to the human gene KIAA0052: emergence of a new gene family.";
Nucleic Acids Res. 23:2120-2126(1995).
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15-JUL-1998 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Helicase SKITW (Helicase-like protein) (HLP).
SKIVZL OR SKIVO OR SKIVO OR DDX13 OR W.
Homo sapiens (Human)
                                                                                EMBL; Z48796; CAA88733.1; AJ EMBL; AF019413; AAB67978.1; EMBL; X98378; CAA67024.1; EMBL; U09877; AAB52523.1; AJ
                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification and characterization of a human cDNA homologous yeast SKI2.";
Genomics 25:660-666(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95278935; PubMed=7759100; Lee S.-G., Lee I., Park S.H., Kang C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=95334363; Dangel A.W., Shen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Hippocampus;
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                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olavesen
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Genew; HGNC: MIM; 600478;

InterPro; IPR001410;

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RESULT
APE1_MC
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Best Local
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P28352;
01-DEC-1992
01-DEC-1992
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
CONFLICT
SEQUENCE
 SEQUENCE
                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                             endonuclease 1) (APEX
                                                                                                                                             01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA-(apurinic or apyrimidinic site) lyase (EC
                                                                                                                                                                                                                                                                MOUSE
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SITE
                                 NCBI_TaxID=10090;
                                                                                          Mus musculus
                                                                                                               APEX OR APE.
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SMART; SM00490; HELICC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                              237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLCVN----VSLGGNEFCLMTSH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPPYCAYLKKRAASYTIITGNEEGYFTAILLKKGRVKF--KSQEIIPFP----NTKMMRN 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQDPQDRGPATAEVPYPD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDAAEPAGPAGRAASAPEAAQAEEDRVKRRRLQCLGFALV---GGCDPTMV------
                                                                                                                                                                                                                                                                                                                                     DQLPNTLKQGIERVRAVAKRIGEVQVACGLNQTVEEFVGELNFGLVEVV 1173
                                                                                                                                                                                                                                                                                                                                                                        --LESTREHSAERIRQLKTVLGKMQEA--PDSTTVIFAGDTNLRDQEVI
                                                                                                                                                                                                                                                                                                                                                                                                              LGYVDEAGTVKLAGRVACAMSSHELLLTELMFDNALSTLRPEEIAALLSGLVCQSPGDAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FP--AQYLKLRER-------MQIQKEMERLRFLLSDQSLLLFPEYHQRVEVLRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITTKVLRVNG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --PSYLRENDWQTQKALSAYFELPENDQGWPRQPPTSFKSEAYYDLTNEDANDTTILEAS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00270;
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FROM N.A
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562
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                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.8%;
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LLVSSPASRAW (IN REF. 4).
R -> Q (IN REF. 3, 4 AND 6).
                                               Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V -> M (IN REF. 2).
RQQPKFKKDPPLAA -> 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAWLPLHGVEHSARKWQRKTDPWSLLAVLGAPVPSDLQAQRHPTTGQILGYKEVL -> QPGCLCMVWSTQPENGRGRRIPG
                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ţ
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                                                                                                                             (APEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      > Q (IN REF. 3, 4 AND 6
> Q (IN REF. 4).
> P (IN REF. 4).
> P (IN REF. 4).
> T (IN REF. 4 AND 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     904405C8C70621A0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----DLVGFKLFLPEGPCDHTVVKLQPGDMAA
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                                                                                                                                                                                                                                             316
                                                                                                                                                                                                                                           AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                    Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ^{\circ}^{\circ}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 131;
                                                                      Euteleostomi;
                                                 Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6)
                                                                                                                                                                                                                                                                                                                                                                          281
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InterPro; IPR000097; APendonclse1.
InterPro; IPR00442; ExoDNase_III.
InterPro; IPR004408; ExoIII_xth.
InterPro; IPR005135; Exo_endo_phos.
InterPro; IPR005135; Exo_endo_phos.
InterPro; IPR00195; Exo_endo_phos.
ITGREAMS; TIGR00195; exoDNase_III; 1.
TIGREAMS; TIGR00195; exoDNase_III; 1.
PROSITE; PS00726; AP_NUCLEASE_F1_1; 1.
                                                                                                                                                                                                                                                                     PIR; S17524; S17524.
PIR; A39500; A39500.
HSSP; P27695; 1BIX.
MGD; MGI:88042; Apex.
                                                              PROSITE;
DNA repair; Lyase; INIT_MET 0
METAL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochim. Biophys. Acta 1079:57-64(1991).

11 FUNCTION: REPAIRS OXIDATIVE DNA DAMAGES IN VITRO. MAY HAVE A ROLE IN PROTECTION AGAINST CELL LETHALITY AND SUPPRESSION OF MUTATIONS. REMOVES THE BLOCKING GROUPS FROM THE 3' TERMINI OF THE DNA STRAND BREAKS GENERATED BY IONIZING RADIATIONS AND BLEOMYCIN.

12 CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or apyrimidinic site in DNA is broken by a beta-elimination reaction, leaving a 3'-terminal unsaturated sugar and a product with a
                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed entities requires a license agreement (See or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (APEX nuclease) with significant homology texonuclease III.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91363416; PubMed=1716153; Seki S., Ikeda S., Watanabe S. H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-129; TISSUB-Embryo;
MEDLINE-95178846; PubMed-7533013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A mouse DNA repair er
apurinic/apyrimidinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          characterization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Ascites;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics
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Apex gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95301294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mamm. Genome 5:717-722(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takiguchi Y., Chen D.J., "Genomic structure of the mouse apurinic/apyrimidinic endonuclease" (x,y) = (x,y) + (y,y)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92041936; PubMed=1939131; Seki S., Akiyama K., Watanabe S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsutsui K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             terminal 5'-phosphate.
SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE AP/EXOA FAMILY OF DNA REPAIR ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                    D90374; BAA14382.1;
U12273; AAC13769.1;
D38077; BAA07270.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K., Nagao K., Oshida
g, sequence analysis,
                                                            PS00726; AP_NUCLEASE_F1_1;
PS00727; AP_NUCLEASE_F1_2;
PS00728; AP_NUCLEASE_F1_3;
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4; PubMed=7782087;
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                                           Nuclear
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titute. There
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hatsushika M.,
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  OR
  MANGANESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as its content
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P23196;
01-NOV-1991
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                                   MEDLINE-87289027; PubMed-2441359;
MEDLINE-87289027; PubMed-2441359;
MEDLINE-87289027; PubMed-2441359;
MEDLINE-87289027; Michael amino acid sequence of an apurinic/apyrimidianic endonuclease from calf thymus.";
Nucleic Acids Res. 15:5529-5544(1987).
IN PROTECTION AGAINST CELL LETHALITY AND SUPPRESSION OF MUTATIONS.
REMOVES THE BLOCKING GROUPS FROM THE 3' TERMINI OF THE DNA STRAND
BREAKS GENERATED BY IONIZING RADIATIONS AND BLEOMYCIN.
IN CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or apyrimidinic site in DNA is broken by a beta-elimination reaction, leaving a 3'-terminal unsaturated sugar and a product with a terminal 5'-phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-(apurinic or apyrimidinic site) lyase (EC endonuclease 1) (APEX nuclease) (APEN).
APEX OR APE OR BAPI.
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"Isolation of cDNA clones encoding an enzyme
repairs oxidative DNA damage in vitro: homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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MEDLINE=91212189; PubMed=1708495;
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                       SUBUNIT: MONOMER (BY
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T FOR SUBSTRATE
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enzyme from bovine cells
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-i- INDUCTION: BY SEVERAL DNA DAMAGING AGENTS.
-i- SIMILARITY: BELONGS TO THE AP/EXOA FAMILY OF DNA REPAIR ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METAL
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                     NCBI_TaxID=584;
                                                         Proteus.
                                                                              Bacteria; Proteobacteria;
                                                                                                             Proteus mirabilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLVTAYVPNAGRGLVRLEYRQRWDEAFR--KFLKGLASRKP----LVLCGDLNVAHEEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----RAWIKKKGL-DWVKEEAPDILCLQETKCSENKLPVELQELSGLSHQYWSAPSD
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ndo_phos; 1.
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MAGNESIUM OR MAGNESE (
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                    subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Best Local
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530865; P75671;
01-JUL-1993 (Rel. 26, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Hypothetical protein yafp.
YAFD OR B0209 OR Z0232 OR ECS0205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Comparative analysis of the cya locus Gram-negative facultative anaerobes."; Biochimie 78:277-287(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000274; Adenylt_cyclse_1.

pfam; pF01295; Adenylate_cycla: 1.

pROSITE; pS01092; ADENYLATE_CYCLASE_1_1;

pROSITE; pS01093; ADENYLATE_CYCLASE_1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphospha-
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-1 FAMILY
                                                       Nishimura K., Komine
Hisano T., Miki T., I
                                                                                                                                                                                       Escherichia coli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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               SEQUENCE FROM N.A
                                                                                                 SEQUENCE FROM N.A.
                                                                                                                               NCBI_TaxID=562,
                                                                                                                                             Escherichia
                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                         Escherichia coli 0157:H7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                           "miki T., Inokuchi H.; (JUL-1992) to the "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           865 AA;
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 MG1655;
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21.8%;
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                                                                                                                                                         gamma subdivision;
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Pred. No. 7;
25; Mismatches
                                           EMBL/GenBank/DDBJ
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                                                                       Kitabatake M., Mathunaga
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EG11650;

yafD.

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EMBL; D12650; BAA02172.1; ALT_INIT.
EMBL; AE000130; AAC73314.1; ...
EMBL; D83536; BAA77880.1; ALT_INIT.
EMBL; U70214; AAB08631.1; ALT_INIT.
EMBL; AE005196; AAG54505.1; ...
EMBL; AE002550; BAB33628.1; ...
EMBL; X60739; ...
EMBL; X60739; ...
EMBL; X50717; J50717...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature
[6]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schramm S., Duncan M.
Davis K., Federspiel
Lashkari D., Lew H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takemoto K., Mori H., Murayama N., Kataoka K., Yano M., Itoh T., Yanamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichihara S., Mizuno T., Makino K., Nakata A., Yura T., Sampei G., Mizobuchi K.; "Systematic sequencing of the Escherichia coli genome: analysis of the 4.0 - 6.0 min (189,987 - 281,416bp) region."; Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92137666; PubMed=1663890;
Kajie S.-I., Ideta R., Yamato I., Anraku Y.;
"Molecular cloning and DNA sequence of dniR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-K12 / W3110;
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MEDLINE=21156231; PubMed=11258796;
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MEDLINE=21074935; PubMed=11206551;
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N., Hyman R., Kalman S., Komp C., Kur
Lin,D., Namath A., Oefner P., Roberts
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Inositol phosphosphingolipids phospholipase C (EC 3.1.
phospholipase C) (IPS-PIC) (Neutral sphingomyelinase)
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CONFLICT 112 112 7-> S (IN REF.
CONFLICT 223 223 R -> G (IN REF.
SEQUENCE 266 AA; 29991 MW; 5F5AD2BOC4CE57
                                                                                                                                                                       MEDLINE-20564359; PubMed=11006294; CHARACTERIZATION.

MEDLINE-20564359; PubMed=11006294; Luberto C.,
                                                                                                                                                                                                                                                     Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Ara Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Che Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smaylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                 STRAIN=S288c / AB972;
Dietrich F.S., Mulligan J.T.,
Aviles E., Berno A., Brennan
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                                                                                                          "Identification of ISC1 (YER019w) as inositol phospholipase C in Saccharomyces cerevisiae.", J. Biol. Chem. 275:39793-39798(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YEAST
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                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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            FUNCTION: Responsible for the hydrolysis of the phosphosphingolipids (IPS), inositol phosphorylecramide (IPC), mannosylinositol phosphorylecramide (MIPS), and mannosyldinositol phosphorylecramide (MIPS)2C). Also active on sphingomyelin, but this activity is probably not physiologically relevant. CQFACTOR: Magnesium.
    SUBCELLULAR LOCATION: Integral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YEAST
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      membrane
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                                                                                                                                                                           Bielawska A.,
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RESULT 15
VTER_HSV7J
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SEQUENCE
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01-OCT-1996
16-OCT-2001
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SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                  NICTION OF THE NICE OF THE BUBL/GenBank/DDBJ databases.

Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOOFFHER HSV-1 UL15,

-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOOFFHER HSV-1 UL15,

HSV-6 ORF12L, EHV-1 44, HCMV UL89, EBV BGRF1/BDRF1, AND VZV 42/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                        Alphaherpesvirinae;
NCBI_TaxID=57278;
                                                                 Nicholas J.;
                                                                                                                                    Viruses; dsDNA viruses, no RNA stage;
                                                                                                                                                 Human herpesvirus (type 7 / strain JI) (HHV7)
                                                                                                                                                                                                                                 P52462;
                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                           Probable DNA packaging protein
                                                                                                                                                                                                                                               VTER_HSV7J
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                                                                                                                                                                                                                                                                                                                                                                    QLHGKQDLAVIARLSPLQQLLKGC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSAERIRQLKTVLGKMQEAPDSTTVIFAGDTNLRDQEVIKCGGLPD-----
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 SWISS-PROT
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lase; Magnesium; Transmembrane
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76; Conservative
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(Rel. 34, Last sequence update)
(Rel. 40, Last annotation updat
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SUBSTRATE RECOGNITION
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Search completed: November 14, 2002, 10:25:48 Job time: 10.5639 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA packaging.
SEQUENCE 663 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR003499; DNA_pack_N.
Pfam; PF02499; DNA_pack_C; 1.
Pfam; PF02500; DNA_pack_N; 1.
DNA_pack_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U43400; AAC54723.1; -.
                                                                                                                                                            341 LTKLSNSPFEMLTVVSYVCEDHVHILNDRGNATTCACYRLHKPKFISINADVKKTADLFL 400
                                                                                      401 EGAFKH 406
                                                                                                                             318 PAAYKH 323
                                                                                                                                                                                                                                                       291
                                                                                                                                                                                                                                                                                                                          233 YVAHQKHVSHFVMKD--VEFKCRRFFPQKNITCQDNVITIEHETIKSTALFASCYNTHSI 290
                                                                                                                                                                                                                                                                                                                                                                                                           181 -YKFDIEFINESSVNILKQKASVFLVPRRHGKTWFMIPVICFLLKN-----LEGISIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 LYSPDVVFLQE-------VIPPYCAYLKKRAASYTIITGNEEG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 RWICGDFENTNKKERIKLE-----PFQKSILIHIIFF----ISVTKLPTLANHVLDYLK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 CDP-----TMVPSVLREN-DWQTQKALSAYFELPENDQGWPRQPPTSFKSEAYV---- 96
                                                                                                                                                                                                                                            RGQSFNLLIVDESHFIKKDAFS-----TILGFLPQS--STKIIFISSTNSGNHSTSF 340
                                                                                                                                                                                                                                                                                 GGNEFCLM----TSHLESTREHSAERIRQLKTYLGKMQEAPDSTTVIFAGDTNLRDQEVIK 282
                                                                                                                                                                                                                                                                                                                                                                   Y-----FTAILLKKGRVKFKSQEIIPFPNTKMMRNLL-------------CVNV-SL 225
                                                                                                                                                                                                              CGGLPDNVFD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76411 MW; 8002D6FA1D166DEC CRC64;
                                                                                                                                                                                                     -----AWEFLGKPKHCQYTWDTKANNNLRI 317
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2002, 10:23:41; Search time 13,8671 Seconds (without alignments) 2565.041 Million cell updates/sec

Title:
Perfect score:
Sequence:

US-09-697-863A-4 1968 1 MASGSSSDAAEPAGPAGRAA.....DCGRFPSDHWGLLCTLNVVL 370

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

esult No. Score	Query		BB		Description
1 432.5 2 275	н К	362 441	NN	T27272 B86252	hypothet
3 118.5	σ.	253	N	ω (55 (hypothetica
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5 105.5	5	267	2	6404	e l'andeny ver de l'annoi e
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9 100.5		502	· ·	T40792	dynein neavy
9		556	N	\$22634	iypociietica
99		678	N	H96552	hvnothetical
	5	1495	N	S27001	alaha-2-macroqlobu
	4.	2218	N	B84683	hypothetical
96	4	840	N	S74707	nitrogen fixation
94.	4.	549	N	T02790	hypothetical
9		1240	Ν	T48800	SMT4 related
9	.4	282	N	T51013	
93.	4.8	1246	2	75	licase
9	4.7	270	N	н83327	
0 9	4.7	317	N	A39500	DNA-(apurinic
1 92.	4.7	288	2	T24066	exonuclease III
. 9	4.	318	2	S26830	DNA-(apurinic
ω 9	4.	266	N	C64745	
4 9	4.	266	N	E90654	
9	4.	266	Ν	E85505	
9		809	N	G87638	ς
7 9	4.	691	Ν	C84300	Cell division cv
28 89.5		477	N	0	+ +
89.	4.	663	N	419	

RESULT 2
B86252
hypothetical protein [imported] - Arabidopsis thaliana

45	44	43	42	41	40	39	38	37	36	ω G	34	ω ω	32	31	30
86.5	87	87	87	87	87.5	88	88	88	88	88.5	88.5	89	89	89.5	89.5
4.4	4.4	4.4	4.4	4.4	4.4	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5
435	875	497	342	259	536	563	362	361	290	1196	838	571	318	923	750
8	N	N	Ν	2	N	N	2	N	2	N	2	N	N	N	N
G84518	н81739	B82981	AC1266	AH0533	AH3227	F64130	A56745	S68268	AC3417	S35994	G84599	н97070	S23550	A86334	AB0708
Mutator-like trans	alanvi-tRNA synthe	probable aldehyde	S-adenosylmethioni	conserved hypothet	geneC protein [imp	qlucose-6-phosphat	microfibril-associ	apurinic/apyrimidi	DNA polymerase, ba	DNA repair protein	probable retroelem	membrane associate	DNA-(apurinic or a		catalase (EC 1.11.

ALIGNMENTS

QY 330 FRAEEGHLIPQSLDLVGLEKL-DCGRFPSDHWGLLCT 365 : :::	Qy 270 AGDTNLRDQEVIKCGGLPDNVFDAWEFLGKPKHCQYTWDTKANNNLRIPAAYKHREDRIF 329 : : ::	Qy 213 KMMRNLLCVNVSLGGNEFCLMTSHLESTREHSAERIRQLKTVLGKNQEAPDSTTVIF 269	Qy 154 SPDVVFLQEVIPPYCAYLKKRAASYTIITGNEE-GYFTAILLKKGRVKFKSQEIIPFPNT 212	Qy 103 ANDTTILEASPSGTPLEDSSTISFITWNIDGLDGCNLPERARGVCSCLALY 153	QY 43 FALVGGCDPTMVPSVLRENDWQTQKALSAYFELPENDQGWPRQPPTSFKSEAYVDLTNED 102 :: : : : : : : : : :	Query Match 22.0%; Score 432.5; DB 2; Length 362; Best Local Similarity 33.5%; Pred. No. 2e-28; Matches 113; Conservative 55; Mismatches 126; Indels 43; Gaps 11;	RESULT 1 T27272 hypothetical protein Y63D3A.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T27272 R;White, S. submitted to the EMBL Data Library, October 1998 A;Reference number: Z20335 A;Accession: T27272 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-362 <wild- a;cross-references:="" a;experimental="" a;genetics:="" a<="" c;genetics:="" cesp:y63d3a.4="" clone="" embl-al033652;="" gspdb:gn00019;="" pidn:caa21707.1;="" source:="" th="" y63d3a=""></wild->
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hypothetical protein SC6E10.19c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: O5-Nov-1999 #sequence_revision O5-Nov-1999 #text_change O5-Nov-1999
C;Accession: T35506
R;Seeger, K; Harris, D; James, K.D.; Parkhill, J; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, August 1999
A;Reference number: Z21580
A;Accession: T35506
A;Accession: T35506
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-253 <SEE>
A;Cross-references: EMBL;AL109661; PIDN:CAB51973.1; GSPDB:GN00070; SCOEDB:SC6E10
A;Experimental source: Strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC6E10.19c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B86252
R;Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.;
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dew ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.;
C.A.; Li, J.H.; Li, Y; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Ma
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; T
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A. Accession: B86252
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Best Local Similarity
Matches 92; Conserv
                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389
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                                                                                                      Local
                                            TILEASP-SGTPLEDSSTISFITWNIDGLDGCNLPERARGVCSCLALYSPDVVFLQEVIP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSLPALPNSRTEPDGSAVIRVLSYNIRSLRD-DTDALARVIKAC----APDLVLLQEA-P 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD----KLDGKFPLPDKWVDVWEVL-KPGDLGFTYDTKANPMLSGNRALQKRLDRILCRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPGRKPLVFATSHLESPCPGPPKWDQMFSRERVEQAKEAIEILR----PNANVIFGGDMNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRKSNWWKAYSCSVSVDVAVSRGYYCMLLSKLGVKSFSSKS---FGNSIMGRELSIAEVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKKR-----AASYTIITGNEEGYFTAILLKKGRVKFKSQEIIPFPNTKMMRNLLCVNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASDSGTPLTCLKILSYNVWFREDLE---LNLRMRAIGHLIQLHSPHLICFQEVTPETYDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDQEVIKCGG---LPDNVFDAWEFLGKPKHCQYTWDTKANNNLRIPAAYKHRFDRIFFRA
                                                                                     Similarity 23.
68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.0%;
                                                                                                      6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 275; DB 2; Length 44
; Pred. No. 4.2e-15;
38; Mismatches 111; Indels
                                                                                   Score 118.5; DB
Pred. No. 0.024;
9; Mismatches 1
                                                                                                                        DB 2;
                                                                                       115;
                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSPDB:GN00141
                                                                                       65;
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                                                                                                                                                                                                                      SCOEDB:SC6E10.19c
                                                                                                                                                                                                                                                                                                                                                  Rajandream,
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275
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R.; Marziali
                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
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                                                                                                                                                                                                                                                                                                                                                    M . A .
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war, K.
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RESULT
H64044
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                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
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A; Residues: 1-252 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                             В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: SMb20092
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: D95853
                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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A;Cross-references: GB:AL591985; PIDN:CAC48492.1; PID:g15139964; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L: Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Proc. Natl. Acad. Sci. U.S.A. 98, 9899-9894, 2001
A;Title: The complete sequence of the 1,683-kb psymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-200:
C;Accession: D95853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) maga C; Species: Sinorhizobium meliloti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 ISFITWNIDGLDGCNLPERARGYCSCLALYSPDVVFLQEV------IPPYCAYL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 IRFLTYNVHSCFGTDRRLDPARIAAVIAECQPDVIALQEVDVGRARTGGIDQAHMIATHL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 21.1
les 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYCAYLKK-----RAASYTIITGNEEGYFTAILLK-KGRVKFKSQEIIPFPNTKMMRNLL 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAVVRIGGARIGVLSSHLSLDAD---ERHEQAGLLLDHL-AALGVKHAVAGGDLNERP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHLIPQSLDLVGLEKLDCG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----GGRTFRRLGEGLRDCW--TAAPWGGEYTFPATAPD-----RRIDAVFVTE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIKCGG-----LPDNVFDAWEFLGKPKHCQYTWDTKANNNLRIPAAYKHRFDRIFFRAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CVNVSLGGNEFCLMTSHLESTREHSAERIRQLKTVLGKMQEAPDSTTVIFAGDTNLRDQE 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RFFRWRKKITRLAAAGDLVLLSGGGTAAGPALLCSLRATVERTEDVLLPLTPGRHRRGIA 116
                                                            GHLIPQSLDLV - - GLEKLDC -
                                                                                                                                                                                               LRDQEVIKCGGLPDNVFDAWEFLGKPKHCQYTWDTKANNNLRIPAAYKHRFDRIFFRAEE 334
                                                                                                                                                                                                                                                                  VIVTHLGL---RGAERLRQATALLGPGWLGGMAQGDAHVVLAGDLNATGRSTAYRLLARQ
                                                                                                                                                                                                                                                                                                                                                                                                     NMEAEFHPALHLEDEKYGDAVLT---ALPMRLIKAAPLPSSSEPRGALWVEIDVAAVKLQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKRAASYTIITGNEEGYFTAILLKKGRVKFKSQEIIPFPNTKMMRNLLCVNVSLGGNEFC 231
                                                                                                                                   LSDAQLL-TGVKPRPTFPS-
                                                                                                                                                                                                                                                                                                                                      LMTSHLESTREHSAERIRQLKTVLGK---MQEAPDSTTVIFAGDTN-
LVGKGIEVASCRVHGSTLARSASDHLPLLAELDVVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GIEVLGCGVPSGLAGVAEDDLRAATDHLPVLTALRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.7%;
21.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 111.5; DB
Pred. No. 0.093;
16; Mismatches 1
                                                                   GREPSDHWGLLCTLNVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -RFPSDHWGLLCTLNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102;
                                                                                                                                          --RLPLL---RIDHV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
   249
                                                                   370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from the N2-fixing
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                                                                                                                                                                                                                                                                             185
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                                                                                                                                          213
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Her

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exodeoxyribonuclease III (EC 3.1.11.2) - Haemophilus influenzae (strain Rd KW20) C;Species: Haemophilus influenzae C;Date: 1B -Aug-1955 #sequence_revision 18-Aug-1995 #text_change 18-Feb-2000 C;Accession: H64044 R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: H64044
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: A97359; PMID:11743194
A;Accession: F97566
A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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                                                                                                                                                                                                                                                                                                                                                                                                                          R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2323-3238, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable nuclease (PA4172) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 *sequence_revision 30-Sep-2001 *text_change 11-Jan-2002
C;Accession: F97566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
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                                         ΔÃ
                                                                                                                                                                                       A; Map position: circular chromosome C; Superfamily: exodeoxyribonuclease III
                                                                                                                                                                                                                                        A; Gene: AGR_C_3151
                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-265 <KUR>
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A;Residues: 1-267 <TIGR>
A;Cross.references: GB:U32689; GB:L42023;
C;Superfamily: exodeoxyribonuclease III
                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE007869;
                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 TGNEEGYFTAILLKKGRVKFKSQEIIPFPNTKMMRNLLCVNVSLGGNEFCLMT----- 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKFISFNINGLRA-----RPHQLEAIIEKYQPDVIGLQEIKVADEAFPYEITENLGYHVF 55
  ū
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGESRAHETKFPAKEKFYADLQQYLEK--EHDKSNPILIMGDMNISPSDLDIGIGDENRK 169
  TWNINGVKA
                                           TWNIDGLDGCNLPERARGYCSCLALYSPDYVFLQEV--IPPYCAYLKKRAASYTIITGNE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAYKHREDRIFFR---AEEGHLIPQSLDLVGLEKLDCGREPSDH 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RWIRTGKCSFLPEERAWYORLYDYGLEDSFRKLNPTANDKFSWFDYRSKGFDDNRGLRI- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HHGQKGHYGVALLTKQEPKV-IRRGFPTDNEDAQKRIIMADLE---TEFGLLTVINGYFP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----KCGGLPD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---SHLESTREHSAERI-ROLKTVLGKMQEAPDSTTVIFAGDTNLRDQEVI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63; Conser
                                                                                               67; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -DHILVSQKLAERCVDVGIALDIRAMEK-----PSDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
RIENLCQWLKDSSPDIVCLQEIKSVDEGFPRLEIEALGYHIETHGQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.4%;
                                                                                                                 5.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
                                                                                             34;
                                                                                                                                                                                                                                                                                    PIDN:AAK87487.1; PID:g15156812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 105.5; D
Pred. No. 0.32;
3; Mismatches
                                                                                       Score 102; DB Pred. No. 0.63; 4; Mismatches
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                                                                                             94;
                                                                                                                                        Length 265
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                                                                                             90;
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                                                                                             Gaps
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                                                                                             16;
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A;Cross-references: GB:AE008688; PIDN:AAL42714.1;
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ъ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: Atu1714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: The Genome of the Natural Genetic A; Reference number: AB2577; PMID:11743193
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160
  220
                                          316 RIPAAYKHRFDRIFFRAEEGHLIPQSLDLVGLEK-LDCGRFPSDH
                                                                                                                                                                                                                                                                                                                                                                                                               128 TWNIDGLDGCNLPERARGVCSCLALYSPDVVFLQEV--IPPYCAYLKKRAASYTIITGNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 RI-----DHLMLSAEAA----DRLQSVEIEKHVRAWEKPSDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 D----AWE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 EGYFTAILLKKGRVKFKSQEI---IPFPNTKMMRNLLCVNVSLGGNEFCLMTSHLESTRE
                                                                                       160 DCHDPRVWEGDALFLPKTRAAFRKLENLGFTDAARATTDAAGLYSFWDYQAGAWPKNNGI
                                                                                                                                                                                   116 PDDPVKYPYKLAWMERLRRFAEDRLAMEE-----PLILAGDYNV------IPE-PF
                                                                                                                                                                                                                                243 HS-----AERIRQLKTVLGKMQEAPDSTTVIFAGDTNLRDQEVIKCGGLPDNVF
                                                                                                                                                                                                                                                                                                                        186 EGYFTAILLKKGRVKFKSQEI---IPFPNTKMMRNLLCVNVSLGGNEFCLMTSHLESTRE 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                     5 TWNINGVKA-----RIENLCQWLKDSSPDIVCLQEIKSVDEGFPRLEIEALGYHIETHGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DCHDPRVWEGDALFLPKTRAAFRKLENLGFTDAARATTDAAGLYSFWDYQAGAWPKNNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDDPVKYPYKLAWMERLRRFAEDRLAMEE-----PLILAGDYNV
                                                                                                                                                                                                                                                                           KGFNGVALLS----KVKPDEVNRGLPGDDADEQARFIEGVFSVEGGAIRVCSLYLPNGNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
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DHLMLSAEAA----DRLQSVETEKHVRAWEKPSDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.2%; Score 102; DB 2; Length 265
23.5%; Pred. No. 0.63;
ative 34; Mismatches 94; Indels
                                                                                                                                      -HCQYT---
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                                                                                                                                      -WDTKA - - - - NNNL
                                            359
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T30299
dynein heavy chain isoty
C;Species: Tripneustes g
C;Date: 22-Oct-1999 #seq
C;Accession: T30299

isotype 7A - sea urchin (Tripneustes gratilla) (fragment)
stes gratilla

#sequence_revision 22-Oct-1999 #text_change 17-Nov-2000

	<pre>protein SPAC9B6.11c - fission yeast hizosaccharomyces pombe c-1999 #sequence_revision 03-Dec-199</pre>	-
	A BITS A CHING THE PLANT	A TOTAL ALTON ON DEATH PROPERTY OF THE REBLUCIOSTS (A) A TOTAL CONTROL OF THE REBLUCIOST OF THE REBLUCIOSTS (A) SERVELLY CASE OF THE CONTROL OF THE REBLUCIOST OF THE REBLUC
A/ACCESSION: 130299	EMBL: U03978; NID: g433384; PID: g433385; PIDN: AAA63592.1 n heavy chain, ciliary 5.1%; Score 101; DB 2; Length 1114; tty 21.4%; Pred. No. 5.8; servative 36; Mismatches 87; Indels 72; Gaps 11; APPEAAQAEEDRVKRRRLQCLGFALVGGCDPTMVPSVLRENDWQTOKALSA 71 :	n heavy chain, ciliary 5.1%; Score 101; DB 2; Length 1114; lity 21.4%; Pred: No. 5.8; Struttive 36; Mismatches 87; Indels 72; Gaps 11; APEAAQAEEDRVKRRRIQCLGFALVGGCDPTMVPSVLRENDWQTQKALSA 71
y; translated from GB/EMBL/DDBJ A	n heavy chain, ciliary 5.1%; Score 101; DB 2; Length 1114; 114%; Pred. No. 5.8; Servative 36; Mismatches 87; Indels 72; Gaps APEAAQAEEDRVKRRRLQCLGFALVGGCDPTWVPSVLRENDWQTQKALSA 71 ETTKDLAKAVAKQCVVFCCSDGLDYIALGK 78 WPRQPPTSFKSEAYVDLTNEDANDTTILEASPSG 115	n heavy chain, ciliary 5.1%; Score 101; DB 2; Length 1114; 11.4%; Pred. No. 5.8; Servative 36; Mismatches 87; Indels 72; Gaps 11; APEANABEDRYKRRIOCIGFALVGGCDPTMYPSVLRENDWGTOKALSA 71
y; translated from GB/EMBL/DDBJ 3IB> FMB1-1107978. NTD-0473784. PID-0433385; PIDN:AAA63592.1	5.1%; Score 101; DB 2; Length 1114; 114 21.4%; Pred. No. 5.8; SETVATIVE 36; MISMATCHES 87; Indels 72; Gaps APEAAQAEEDRVKRRRLQCLGFALVGGCDPTMVPSVLRENDWQTQKALSA 71 ETTKDLAKAVAKQCVVFNCSDGLDYIALGK 78 WPRQPPTSFKSEAYVDLTNEDANDTTILEASPSG 115	n heavy chain, ciliary 5.1%; Score 101; DB 2; Length 1114; servative 36; Mismatches 87; Indels 72; Gaps 11; APERAOAREDRYKRRIQCIGFLIVEGEDTHYPSYLKENDWOTOKALSA 71SCPDEPNRIDLEVISVOAGOLD
y; translated from GB/EMBL/DDBJ A GTB> EMBD:U03978; NID:g433384; PID:g433385; PIDN:AAA63592.1	5.1%; Score 101; DB 2; Length 1114; 114%; Pred. No. 5.8; Servative 36; Mismatches 87; Indels 72; Gaps APEAAQAEEDRYKRRRLQCLGFALVGGCDPTMYPSVLRENDWQTGKALSA 71 ETTKDLAKAVAKQCVVFNCSDGLDYIALGK 78 WPROPPTSFKSEAYVDLTNEDANDTTILEASPSG 115	S.18; Score 101; DB 2; Length 1114; 5.18; Score 101; DB 2; Length 1114; servative 36; Mismatches 87; Indels 72; Gaps 11; servative 36; Mismatches 11; servative 36; Mismatches 87; Indels 72; Gaps 11; servative 61; Mismatches 154; Indels 188 SCFDERNEDLEVLSVVAQOILTIGRGINGA-DTULEEG 128 servative 61; Mismatches 154; Indels 189; Gaps 18; servative 61; Mismatches 154; Indels 183; Gaps 18; servative 61; Mismatches 154; Indels 184; servative 61; Mismatches 154; Indels 184; servative
y; translated from GB/EMBL/DDBJ A GIB> EMBL:U03978; NID:g433384; PID:g433385; PIDN:AAA63592.1	S.1%; Score 101; DB 2; Length 1114; Similarity 21.4%; Pred. No. 5.8; Length 1114; Conservative 36; Mismatches 87; Indels 72; Gaps PAGRASAPEAAQAEEDRVKRRRLQCLGFALVGGCDPTMVPSVLRENDWQTQKALSA 71	S.1%; Score 101; DB 2; Length 1114; 31.4%; Pred. No. 5.8; 3); Conservative 36; Mismatches 87; Indels 72; Gaps 11; 2); Capsarabaeaaaebbrykreracyccopthypsylrenbwqrokalsa 71
DN:AAA63592.1	AGRAASAPEAQAEEDRYKRRRLQCLGFALVGGCDPTMVPSVLRENDWQTOKALSA	PROGRAMSAPERANABEDRYKRRRLOCLGEALVGGCDPTWPESVLRENDWQTOKALSA 71
y; translated from GB/EMBL/DDBJ A GIB> GIB> n heavy chain, ciliary 5.1%; Score 101; DB 2; Length 1114; ity 21.4%; Pred. No. 5.8; servative 36; Mismatches 87; Indels 72; Gaps 11;	PAGTGKTYIALGK PAGTGKTYIALGK LPENDQGWPRQPDTSFKSEAYVDLTNEDANDTTILEASPSG	ANGROKAPELANA PROCESSION ANALOGUES ANGROKY
y; translated from GB/EMBL/DDBJ A SIB> GIB> n heavy chain, ciliary n heavy chain, ciliary 5.1%; Score 101; DB 2; Length 1114; ity 21.4%; Pred. No. 5.8; servative 36; Mismatches 87; Indels 72; Gaps 11; APEAAOAEEDRYKRRRLOCLGFALVGGCDPTMYPSVLRENDWQTQKALSA 71	LPENDOGWPROPPTSFKSEAYVDLTNEDANDTTILEASPSG	LDENDOGMPROPPTSEKSEAYVDLTNEDANDTTLEASPSG 115 ELASCGAWSCPEDENRIDLEVLSVVAQQILTIORGINAGA-DTILLEEG 128 EDSSTIS-FITWNIDGLDGCNLPERARGUCSCLALYSPDVVFIQEVIPYCAYLKKR 174
y; translated from GB/EMBL/DDBJ A A GIB> GIB> n heavy chain, ciliary n heavy chain, ciliary 5.1%; Score 101; DB 2; Length 1114; ity 21.4%; Pred. No. 5.8; servative 36; Mismatches 87; Indels 72; Gaps 11; appaaQaeeDRVKRRRLQCLGFALVGGCDPTMVPSVLRENDWQTOKALSA 71 ::	LPENDQWPRQPPTSFKSEAYDLTREDANTTILEAPSG	LENDOGRPROPPTSFKSEAVDLTIBOANUTILLEASPOG 113 LEASCGAWSCEDEFNRIDLEVLSVVAQQILTIQRGINAGA-DTLLFEG 128 EDSSTIS-FITWNIDGLDGCNLPERARGVCSCLALYSPDVVFLQEVIPPYCAYLKKR 174
y; translated from GB/EMBL/DDBJ A A SIB> SIB> EMBL:U03978; NID:9433384; PID:9433385; PIDN:AAA63592.1 n heavy chain, ciliary 5.1%; Score 101; DB 2; Length 1114; ity 21.4%; Pred. No. 5.8; servative 36; Mismatches 87; Indels 72; Gaps 11; APEAAQAEEDRVKRRRLQCLGFALVGGCDPTMVPSVLRENDWQTOKALSA 71	EDSSTIS-FITWNIDGLDGCNLPERARGVCSCLALYSPDVVFLQEVIPPYCAYLKKR :	EDSSTIS-FITWNIDGLDGCNLPERARGUCSCLALYSPDVFLOEVIPPYCAYLKKR 174
y: translated from GB/EMBL/DDBJ A 31B> SIB> n heavy chain, ciliary 5.1%; Score 101; DB 2; Length 1114; ity 21.4%; Pred. No. 5.8; Indels 72; Gaps 11; servative 36; Mismatches 87; Indels 72; Gaps 11; apEAAQAEEDRVKRRRLQCLGFALVGCDPTMVPSVLRENDWQTQKALSA 71ETTKDLAKAVAKQCVVFNCSDGLDYIALGK 78 WPRQPPTSFKSEAYVDLTNEDANDTTILEASPSG 115		KLDPTCSVFITMNPGYAGRSDLEPDNLKALFRTVANMYDDYALISEIVLYSCGETKAR 188 KLDPTCSVFITMNPGYAGRSDLEPDNLKALFRTVANMYDDYALISEIVLYSCGETKAR 188 YTTITGNEEGYFTAILLKKGTVFFKSQEIIPFPNTKMM 215 : :
Y: translated from GB/EMBL/DDBJ A GIB> GIB> CIBEL:U03978; NID:g433384; PID:g433385; PIDN:AAA63592.1 n heavy chain, ciliary 5.1%; Score 101; DB 2; Length 1114; ity 21.4%; Pred. No. 5.8; servative 36; Mismatches 87; Indels 72; Gaps 11; APEAAQAEEDRVKRRLQCLGFALVGGCDPTMVPSVLRENDWQTOKALSA 71 :	YTIITGREEGYFTAILLKKGRVKFKSQEIIPFDNIKMM :	YVIITGNEEGYFTAILLKKGRVKFKSQEIIPFPNTKMM 215
Y: translated from GB/EMBL/DDBJ A A A B B B B B B B B B B	HCVNV 223 : ICVNV 223	LCVNV 223
Y: translated from GB/EMBL/DDBJ A A A SIB> BMBL:U03978; NID:g433384; PID:g433385; PIDN:AAA63592.1 EMBL:U03978; NID:g433384; PID:g433385; PIDN:AAA63592.1 10.	NDVNL 250	protein SPAC9B6.11c - fission yeast (Schizosaccharomyces pombe) figoraccharomyces pombe c-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000 f140792 aljandream, M.A.; Barrell, B.G.; Volckaert, G. the EMBL Data Library, May 1999 umber: 221875 f140792 liminary; translated from GB/EMBL/DDBJ pe: DNA c-02 <
A SIB> A SIB> A SIB> A SIB> B SIB> B SIB> D SIB> SIB> SIB> SIB> SIB> SIB> SIB> SIB>		protein SPAC9B6.11c - fission yeast (Schizosaccharomyces pombe) hizosaccharomyces pombe c-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000 T40792 ajandream, M.A.; Barrell, B.G.; Volckaert, G. the EMBL Data Library, May 1999 umber: 221875 T40792 lininary; translated from GB/EMBL/DDBJ pe: DNA -502 <woo> ences: EMBL:AL049769; PIDN:CAB42372.1; GSPDB:GN00067; SPDB:SPAC9B6.11c nn: 2 [] 1 source: strain 972h-; cosmid c9B6 SPAC9B6.11c -5.1%; Score 100.5; DB 2; Length 502; Similarity 18.1%; Pred. No. 2.1; Similarity 18.1%; Pred. No. 2.1; B; Conservative 61; Mismatches 154; Indels 183; Gaps 18; TOKALSAYFE</woo>
Translated from GB/EMBL/DDBJ A A A A B B B B B B B Selvative chain, ciliary 5.1%; Score 101; DB 2; Length 1114; 114 21.4%; Pred. No. 5.8; Servative 36; Mismatches 87; Indels 72; Gaps 11; APEAAQABEDRVKRRRLQCLGFALVGGCDPTWVPSVLRENDWQTQKALSA 71		may 1999 Reference number: Z21875 Reference number: Z21875 Accession: T40792 Accession: T40792 Molecule type: DNA Molecule type: DNA Molecule type: DNA Molecule type: DNA Residues: 1-502 <mood> Cross-references: EMBL.AL049769; PIDN:CAB42372.1; GSPDB:GN00067; SPDB:SPAC9B6. Residues: 1-502 <mood> Cross-references: EMBL.AL049769; PIDN:CAB42372.1; GSPDB:GN00067; SPDB:SPAC9B6. Cross-references: EMBL.AL049769; PIDN:CAB42372.1; GSPDB:GN00067; SPDB:GN00067; SPDB:SPAC9B6. Cross-references: EMBL.AL049769; PIDN:CAB423</mood></mood>
TABLE OF THE PROPERTY OF THE P	T40792 ajandream, M.A.; Barrell, B.G.; Volckaert,	;Accession: 140/92 ;Status: preliminary; translated from GB/EMBL/DDBJ ;Status: preliminary; translated from GB/EMBL/DDBJ ;Molecule type: DNA ;Residues: 1-502 <moo> ;Residues: 1-502 <moo> ;Residues: 1-502 <moo> ;Cross-references: EMBL:AL049769; PIDN:CAB42372.1; GSPDB:GN00067; SPDB:SPAC9B6. ;Cross-references: EMBL:AL049769; DB 2; Length 502; ;Adap position: 2</moo></moo></moo>
A SIBS SIBS A NEWBL:U03978; NID:9433384; PID:9433385; PIDN:AAA63592.1 EMBL:U03978; NID:9433384; PID:9433385; PIDN:AAA63592.1 1	740792 ajandream, M.A.; Barrell, B.G.; Volckaert, the EMBL Data Library, May 1999 umber: Z21875	;Residues: 1-502 <woo>;Cross-references: EMBL:AL049769; PIDN:CAB42372.1; GSPDB:GN00067; SPDB:SPAC9B6.;Cross-references: EMBL:AL049769; PIDN:CAB42372.1; GSPDB:GN00067; SPDB:SPAC9B6.11c;Cross-references: EMBL:AL049769; PIDN:CAB42372.1; GSPDB:GN00067; SPDB:SPAC9B6.11c;Cross-references: SPDB:SPAC9B6.11c ;Gene: SPDB:SPAC9B6.11c ;Map position: 2 ;Introns: 76/1 ;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC9B6.11c ;Superfami</woo>
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A THEMBL: U03978; NID: g433384; PID: g433385; PIDN: AAA63592.1 SIBY 5.1%; Score 101; DB 2; Length 1114; \$5.1%; Score 101; DB 2; Length 1114; \$14 21.4%; Pred. No. 5.8; SETVATIVE 36; MISMATCHES 87; Indels 72; Gaps 11; APPEAQABEDRVKRRRLQCLGFALVGGCDPTWVPSVLRENDWQTQKALSA 71	T40792 ajandream, M.A.; Barrell, B.G.; Volckaert, G. the EMBL Data Library, May 1999 umber: Z21875 T40792 11minary; translated from GB/EMBL/DDBJ pe: DNA -502 <woo> ences: EMBL:AL049769; PIDN:CAB42372.1; GSPDB:GN00067; SPDB:SPAC9B6.1 source: strain 972h-; cosmid c9B6 1 source: strain 972h-; cosmid c9B6 SPAC9B6.11c n: 2 //1 : Schizosaccharomyces pombe hypothetical protein SPAC9B6.11c</woo>	62 DWQTQKALSAYFELPENDQGWDRQPPTSFKSEAYVDLTNEDANDTTILEAS 1 :: :: :: :: :
A SIBN- SIBN- SIBN- SIBN- DIBY: NID:9433384; PID:9433385; PIDN:AAA63592.1 EMBL:U03978; NID:9433384; PID:9433385; PIDN:AAA63592.1 n heavy chain, ciliary 5.18; Score 101; DB 2; Length 1114; 112, 21.48; Pred. No. 5, 8; Indels 72; Gaps 11; APEAAAAEDENKKRRIQCIGFALVGGCDFTMVPSVLRENDWOTOKALSA 71	ajandream, M.A.; Barrell, B.G.; Volckaert, G. the EMBL Data Library, May 1999 umber: 221875 T40792 liminary: translated from GB/EMBL/DDBJ pe: DNA -502 <woo> ences: EMBL:AL049769; PIDN:CAB42372.1; GSPDB:GN00067; SPDB:SPAC9B6. 1 source: strain 972h-; cosmid c9B6 1 source: strain 972h-; cosmid c9B6 : SPAC9B6.11c n: 2 n: 2 n: 2 Schizosaccharomyces pombe hypothetical protein SPAC9B6.11c : Schizosaccharomyces pombe hypothetical protein SPAC9B6.11c : Similarity 18.1%; Score 100.5; DB 2; Length 502; Similarity 18.1%; pred. No. 2.1; Similarity 18.1%; pred. No. 2.1; Indels 183; Gaps 18;</woo>	113PSGTPLE
Y: translated from GB/EMBL/DDBJ ACTION BMBL:U03978; NID:9433384; PID:9433385; PIDN:AAA63592.1 EMBL:U03978; NID:9433384; PID:9433385; PIDN:AAA63592.1 In heavy chain, ciliary 5.1%; Score 10; DB 2; Length 1114; ity 21.4%; Pred. No. 5.8; Servative 36; Mismatches 87; Indels 72; Gaps 11; APEAAQAEEDRVRRRLQCCLEFALVGCCDPTWVESVLRENDWQTQCKALGA 71	ajandream, M.A.; Barrell, B.G.; Volckaert, G. the EMBL Data Library, May 1999 under: 221875 T40792 T40792 liminary; translated from GB/EMBL/DDBJ pe: DNA pe: DNA pe: DNA pe: DNA pe: DNA po: SMBL:AL049769; PIDN:CAB42372.1; GSPDB:GN00067; SPDB:SPAC9B6. l source: strain 972h-; cosmid c9B6 l source: strain 972h-; cosmid c9B6 l source: strain 972h-; cosmid c9B6 l source: strain 972h-; DB 2; Length 502; spac9B6.llc cn: 2 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	81 RKPIAPPSNAPPEFNTDFIKREMLSIPNYAPFETEKSALDITIMTYNVLAQTNIRRSM 1.0
Y: translated from GB/EMBL/DDBJ 31B> 31B> 31B> 31B> 31B> 31B> 31B> 31B>	THAOT92 ajandream, M.A.; Barrell, B.G.; Volckaert, G. the EMBL Data Library, May 1999 umber: Z21875 T40792 liminary; translated from GB/EMBL/DDBJ pe: DNA -502 <wood- 100.5;="" 18.18;="" 2.1;="" 2;="" 5.18;="" 502;="" db="" embl:al049769;="" ences:="" gspdb:gn00067;="" length="" no.="" pidn:cab42372.1;="" pred.="" score="" similarity="" spac9b6.11c="" spdb:spac9b6.11c="" stokalsayfe<="" td=""><td>140PERARGYCSCLALYSPDYVFLQEVIPPYCAYLKKRAASYTIITGN</td></wood->	140PERARGYCSCLALYSPDYVFLQEVIPPYCAYLKKRAASYTIITGN
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A;Title: The primary sequence and the subunit structure of mouse alpha-2-macroglobulin, A;Reference number: $27001; MUID:93076803; PMID:1280217
A;Recession: $27001
A;Recession: $27001
A;Molecule type: mRNA
A;Residues: 1-1495 (LEU)
A;Residues: 1-1495 (LEU)
A;Cross-references: EMBL:M93264; NID:9199085; PIDN:AAA39508.1; PID:9199086
A;Cross-references: EMBL:M93264; NID:93085; PIDN:AAA39508.1; PID:9199086
A;Cross-references: EMBL:M93264; NID:93085; PID:7528166
A;Accession: A55002; MUID:95095249; PMID:7528166
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A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: 196552
                                                                                                                                                                                                                                                                                                                       alpha-2-macroglobulin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S27001; A55002
R;van Leuven, F; Torrekens, S.; Overbergh, L.; Lorent, K.; de Strooper, B.
Bur. J. Bjochem. 210, 319-327, 1992
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A;Molecule type: DNA
A;Residues: 1-678 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F5D21.8 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C;Paccession: H96552 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H
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Best Local Similarity
Matches 61; Conserv
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20.7%;
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Pred. No. 3
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A; Molecule type: DNA
A; Residues: 1-40, 'SGIPEKA', 48-159 <1
A; Cross-references: GB:U06977
A; Note: authors translated the codor and GCC for residue 47 as Pro C; Genetics: 4; Introns: 29/2; 92/3; 144/1
C; Superfamily: alpha-2-macroglobulin
Qy
                                       В
                                                                        QY
                                                                                                                  В
                                                                                                                                                     QΥ
                                                                                                                                                                                            B
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: B84683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein At2g28300 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: B84683
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                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-2218 <STO>
                                                                                                                                                                                                                                                                                                                                                                        A; Gene: At2g28300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 AQAEEDRVKRRRLQCLGFALVGG------CDPTMVPSVLREND---WQTQ------KALS
                                                                                                                                                                                                                                                                                                Local
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    PN-TKMMRNLL-
                                         ----HLPPSAEPDGDIHVHLKETEKSESMVVVGEGTAFPSSLPVTEEGNAESQLADTEPF
                                                                              FLQEVIPPYC----
                                                                                                                    SQLANIEPSSSP---
                                                                                                                                                   TTILEASPSGTPLEDSSTISFITWNIDGLD------GCNLPERARGVCSCLALYSPDVV 158
                                                                                                                                                                                            GGCG---LVDVLTECSSEPQ------LQLPPS-----AEPVISEGTELATLPLTEEENAD 1835
                                                                                                                                                                                                                                    GGCDPTMVPSVLRENDWQTQKALSAYFELPENDQGWPRQPPTSFKSE-AYVDLTNEDAND 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQSQESHVYTKALLAYAFALAGNKAKRSELLESLNKDAVKEEDSLHWQRPGDVQKVKALS 1208
                                                                                                                                                                                                                                                                           74; Conserv
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                                                                                                                  ----SVVEKNIEAQDQDQVKTAGCELVSTG----CSS----EPQV-
                                                                                                                                                                                                                                                                                              4.98;
21.48;
                                                                            -AYLKKRAASYTIITGNEEGYFTAIL--LKKGRVKFKSQEIIPF
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-CVNVSLGGN----EFCLMTSHLESTREHSAERIRQLK
                                                                                                                                                                                                                                                                         Score 97; DB Pred. No. 34; S3; Mismatches
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Pred. No.
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4; Mismatches
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RESULT 14
$74707
synechocys
nitrogen fixation positive activator protein - Synechocys
N; Alternate names: protein slr1305
C; Species: Synechocystis sp.
A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text.
C; Accession: $74707
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu,
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Ponaka, Res. 3, 109-136, 1996
DNA Res. 3, 109-136, 1996
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C;Superfamily: response regulator homology
C;Keywords: phosphoprotein
F;9-120/Domain: response regulator homology <RRH>
F;57/Binding site: phosphate (Asp) (covalent) #st
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hypothetical protein L549.2 [imported] - Leishmania major (strain Friedlin) C; Species: Leishmania major (c; Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000 C; Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000 C; Accession: B81455; T02790 T; Hixson, G; Kiser, P.; Lemley, C: 1 R; Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G; Kiser, P.; Lemley, C: 1 Proc. *Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999 A; Titley-Leishmania major Friedlin chromosome 1 has an unusual distribution A; Reference number: A81455; MUID:99178987; PMID:10077609
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A; Residues: 1-840 <KAN>
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A; Status: nucleic acid sequence not shown;
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                                                                                                                                                                                                                                                                                                                                          LMWKTLASGRNWHGEFHNRRKNGELYWERASISPISNQQGIVTHYVAVKEDITKEKQQAE
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                                                                                                                                                                                                                                                           ALFHQAHYDHLTGLPNRILAKDRLQQAIESALRQKHIFGLMFLDLDNF 452
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55; Conserv
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nabe, A.;
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                                                                      Lemley, C.; Magness,
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C;Superfamily: Lersumanta
C;Keywords: transmembrane
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A; Map position: 1
C; Superfamily: Leishmania major probable membrane
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE001274; NID:g3264850; PIDN:AAC24614.1; A;Experimental source: strain MHOM/IL/81/Friedlin
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A; Residues: 1-549 < PYL>
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A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                FK-----SEAYVDLTNED------SP 113
                                                                                                                                                                                                                                                                                                                                                               GGPVVGLMRDTGTRTTIRPSIM----DAQIAQSALEVKMSSLLAREMQAEKMEAEREPPLK 73
                                                                                                                    FPLMMPGRDIGQRFHFAHFVGMRDKVTNMTLYVACVQLTAGA-----TAEAADVRLHEA
                                                                                                                                                                               NTELWRYVRFLGYGTLYOSSRGAQVRALRKGDNAAAPSNOGKIAEEEDIGNVLLFHKGRF 242
 AWHYRDDARAAAYDTYYTKNVE-
                                                           RQVLTILDALGRNDADRSHQSHIVCGDLNNQADDEPCVEL--LRDRFFSTHDLVGGPRWT
                                                                                       ERIRQLKTVLGKMQEAPDSTTVIFAGDTNLR--DQEVIKCGGLPDNVFDAWEFLGKPKHC 303
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79; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                               ---TWDTKANNNLRIPAAYKHRFDRIFFRAEEGH
                                                                                                                                                 -KFKSQEIIPFPN--TKMMRNLLCVNVSLGGNEFCLMTSHLESTREHSA 245
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19.7%;
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   -QAHRSDKAYQAEEEIH
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Search completed: November 14, 2002, 10:28:20 Job time: 18.8671 secs

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2: /SIDS2/gcgdata/g:
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AAM39841
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1646.697 Million cell updates/sec
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                                    Human colon cancer
Human protein sequ
Topoisomerase II b
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Human CD40 recepto
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4.4	4.4	4.4	4.4							4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.6	4.6		4.8	4.8			6.4		14.0	14.0	14.0	14.0	14.0	4	20.8
1681 1709	1557	342 710	577	354	668	2253	1703	1284	1284	1284	1284	945	524	345	318	750	1011	747	319	1006	551	474	816	449	76	441	437	426	426	404	404	161
22 22	22	ν ν ω	22	22	21	21	22	22	22	22	22	22	19	21	18	22	22	22	16	23	22	23	22	22	20	21	21	21	21	21	21	20
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ALIGNMENTS

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RESULT 1
AAY56020
tumour necrosis factor; TNF; receptor; superfamily; CD30; homology; TNF receptor associated factor; TRAF; modulator; signalling pathway; diagnosis; NF-kappaB; Jun; kinase; atherosclerosis; multiple sclerosis; arthritis; systemic lupus erythematosus; graft rejection; allergy; graft versus host disease; autoimmune disease.
                                                                                                                                                                                                                                                                                          Antiarteriosclerotic; antiarthritic; neuroprotective; dermatological; immunosuppressive; antiinflammatory; immunosuppressive; antiallergic; human; CD40 receptor associated protein; CRAP; cytoplasmic domain;
           Pype SMC,
                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                      Mouse CD40 receptor associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                  AAY56020;
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                                         (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
                                                                       29-APR-1998;
                                                                                                                                04-NOV-1999
                                                                                                                                                            WO9955859-A2
                                                                                                                                                                                                                                                                                                                                                                                 15-MAR-2000 (first entry)
                                                                                                   28-APR-1999;
           Remacle JEFJG, Huylebroeck DFE;
                                                                       98EP-0201392.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Antiarteriosclerotic; antiarthritic; neuroprotective; dermatological; Anmunosuppressive; antiaflammatory; immunosuppressive; antiaflammatory; immunosuppressive; antiaflammatory; immunosuppressive; antiaflammatory; cRAP; cytoplasmic domain; human; CD40 receptor associated protein; CRAP; cytoplasmic domain; tumnour necrosis factor; TNF; receptor; superfamily; CD30; homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel proteins used to treat inflammatory diseases, NF-kappaB diseases and for improvement of anti-tumor treatments -
                                                                                          Human CD40 receptor associated protein.
                                                                                                                                   15-MAR-2000
                                                                                                                                                                                                             AAY56019 standard; Protein; 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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N-PSDB; AAZ47119.
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1 GLLCTLNVVL 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSTISFITWNIDGLDGCNLPERARGVCSCLALYSPDVVFLQEVIPPYCAYLKKRAASYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NDWQTQKALSAYFELPENDQGWPRQPPTSFKSEAYVDLTNEDANDTTILEASPSGTPLED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MASGSSSDAAEPAGPAGRAASAPEAAQAEEDRVKRRRLQCLGFALVGGCDPTMVPSVLRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 AA;
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                                                                                                                                 (first
                                                                                                                                 entry)
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Pred. No. 1.9e-183;
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This sequence represents the human CD40 receptor associated protein CC (CRAP). CRAP is a functional protein capable of interacting with the Cytoplasmic domain of CD40 and/or other receptors of the tumour necrosis factor (TNF) receptor superfamily such as CD30 and TNF receptor I, where the protein has no homology to TNF receptor associated factor (TRAF) CC proteins. The CD40 binding proteins can be used as modulators of the CD40 signalling pathway, especially to diagnose and treat TRAF-related, CC CD40-related, NF-kappaB related and/or Jun (kinase)-related diseases, and for the improvement of anti-tumour diseases. Diseases which may be treated include atherosclerosis, arthritis, multiple sclerosis, systemic lupus erythematosus, graft rejection, graft versus host disease, allergy, and autoimmune disease. The proteins can be used to sensitize tumour cells to anti-tumour treatments and to screen for compounds which interaction of the proteins with other protein components of the TRAF, CD40 or NF-kappaB related pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNF receptor associated factor; TRAF; modulator; signalling pathway; diagnosis; NF-kappaB; Jun; kinase; atherosclerosis; multiple sclerosis; arthritis; systemic lupus erythematosus; graft rejection; allergy; graft versus host disease; autoimmune disease.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                              Novel proteins used to treat diseases and for improvement
                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (VLAA-) VLAAMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-APR-1999;
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362 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huylebroeck DFE;
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  of anti-tumor treatments -
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Best Local :
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KHRFDRIFFR--AEEGHLIPQSLDLVGLEKLDCGRFPSDHWGLLCTLNVVL 370
                                                                                                                                                                                     RARGVCSCLALYSPDVVFLQEVIPPYCAYLKKRAASYTIITGNEEGYFTAILLKKGRVKF 201
                                                                                                                                                                                                                                    ERRPETISEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWNIDGLDLNNLSE 131
                                                                                                                                                                                                                                                       PRQPPTSFKSEAYVDLTNEDANDTTILEASPS-GTPLEDSSTISFITWNIDGLDGCNLPE 141
                                                                                                                                                                                                                                                                                                                                  EAAQAE-EDRVKRRRLQCLGFALVGGCDPTMVPSVLRENDWQTQKALSAYFELPENDQGW
                                          PESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWDTQMNSNLGITAAC
                                                          PDSTTVIFAGDTNLRDQEVIKCGGLPDNVFDAWEFLGKPKHCQYTWDTKANNNLRIPAAY
                                                                                                        KSQEIIPFPSTKMMRNLLCVHVNVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQEA
                                                                                                                                       KSQETIPFPNTKMMRNLLCVNVSLGGNEFCLMTSHLESTREHSAERIRQLKTVLGKMQEA
                                                                                                                                                                    RARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSSNYEIITGHEEGYFTAIMLKKSRVKL
                                                                                                                                                                                                                                                                                                   EAAEEEGEPEVKKRRLLCVEFASVASCDAAVAQCFLAENDWEMERALNSYFEPPVEESAL 71
                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
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                                                                                                                                                                                                                                                                                                                                                                                 63.9%;
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; Pred. No. 4.2e-114;
43; Mismatches 64;
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312

KLRFDRIFFRAAAEEGHIIPRSLDLLGLEKLDCGRFPSDHWGLLCNLDIIL 362

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Query Match
Best Local S
Matches 240
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
19-JUL-2000;
14-SEP-2000;
                                                                                                             system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                   The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polypucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang
                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and such as central nervous
                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                Note: The sequence specification.
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TYT,
                                                                                           disorders.
The sequen
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                Similarity
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Zhou P,
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                                                      362
    Conservative
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2000US-0662191.
2000US-0693036.
2000US-0727344.
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2000US-0552317.
2000US-0598042.
2000US-0620312.
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Wehrman T,
                                                                                           data
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                63.9%;
                                                                                                                                                                                                                                                                                                                            polypeptides, useful for treating
system injuries -
                                                                                          for this patent did not form part
    43;
               Pred. No. 4.2e-114;
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Xu C, Xue
                           Score 1258; DB 22;
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 Mismatches
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Yang Y,
  64;
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 Indels
                         Length
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Zhang J;
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Gaps
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Qy

24 EAAQAE-EDRVKRRRLQCLGFALVGGCDPTMVPSVLRENDWQTQKALSAYFELPENDQGW

The invention relates

human nucleic acids (AAI57798-AAI61369)

and

Example 2;

SEQ

IJ

6558; to

10078pp; English.

Novel nucleic acids and

nervous NO

polypeptides, useful
system injuries -

for

treating

disorders

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RESULT 4
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25-APR-2000;
09-JUL-2000;
                                                                                                         Wang
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                                                                             WPI; 2001-442253/47.
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03-AUG-2000;
                                                                   N-PSDB; AAI60783.
                                                                                                                                       (HYSE-) HYSEQ INC
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                                                                                               ΥΤ,
QA,
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                                                                                             , Liu C,
Wang Z,
Zhou P,
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2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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2000US-0552317
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Wehrman T,
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, Xu C, Xue AJ,
R, Drmanac RT;
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Zhang
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RESULT 5
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  WPI; 1999-257704/22
                                                                                                                                                                                                                                                                                                 JP11075856-A
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                                                                                                                                                                                                                                                                                                                                                                                                           Topoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY03182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY03182 standard;
                                                     (CHUS ) CHUGAI
(TSUR/) TSURUO
                                                                                                                                      17-SEP-1997;
                                                                                                                                                                                         17-SEP-1997;
                                                                                                                                                                                                                                              23-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Topoisomerase II binding protein
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                                                                                                                                                                                                                                                                                                                                                      sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWDTQMNSNLGITAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 AA;
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                                                        PHARM CO LTD
T.
                                                                                                                                      97JP-0251544
                                                                                                                                                                                            97JP-0251544
                                                                                                                                                                                                                                                                                                                                                                                                           binding protein; TopBP; anticancer agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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RESULT 6
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAX28153
                                                                                                                                                                                                                                                                                                                                                                                                   neural disorder; immune system disorder; muscular disorder;
reproductive disorder; gastrointestinal disorder; renal dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulne; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB53403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB53403 standard;
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                                                                                                                                                         08-MAR-2000; 2000WO-US05883
                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human colon cancer antigen protein sequence SEQ ID NO:943
                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                              21-SEP-2000
                                                                                                       12-MAR-1999;
                                                                                                                                                                                                                                                                   ₩O200055351-A1
                                                                                                                                                                                                                                                                                                                                                                             infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 EAAEEEGEPEVKKRRLLCVEFASVASCDAAVAQCFLAENDWEMERALNSYFEPPVEESAL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 EAAQAE-EDRYKRRRLQCLGFALVGGCDPTMYPSYLRENDWQTQKALSAYFELPENDQGW 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392 AA;
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                                                                                                       99US-0124270
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68.4%;
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Pred. No. 4.7e-114;
13; Mismatches 64;
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DT 26-J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACC AACS97991 to AACS8763 encode the human colon cancer associated proteins, CC called human colon cancer antigens, given in AABS3234 to AABS4006. The CALLED Human colon cancer antigens, given in AABS3234 to AABS4006. The CC called human colon cancer antigens can have cytostatic, cardioactive, muscular; CC current colon cancer antigens polynucleotides, and CC can be used in gene therapy. The colon cancer antigen polynucleotides, and CC can be used in gene therapy. The colon cancer antigen polynucleotides, colon cancer antigen polynucleotides, colon cancer and disprostics and research, such as for CC cancer and disprostics of colon disorders, such as colon cancer. The CC polynucleotides may be used in disprostics and research, such as for CC cancer disorders, muscular disorders, reproductive disorders, immune CC system disorders, muscular disorders, reproductive disorders, immune CC gastrointestinal disorders, wounds, renal disorders, infectious CC daaBs4007 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
 EP1074617-A2
                                 Homo sapiens
                                                                                                     Human protein
                                                                                                                                                                            AAB93674;
                                                                                                                                         26-JUN-2001
                                                                                                                                                                                                           AAB93674 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colon cancer associated gene sequences, referred antigens, useful for the treatment, prevention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 1508-1509; 2104pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                      319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 EAAQAE-EDRVKRRRLQCLGFALVGGCDPTMVPSVLRENDWQTQKALSAYFELPENDQGW 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                               KLRFDRIFFRAAAEEGHIIPRSLDLLGLEKLDCGRFPSDHWGLLCNLDIIL
                                                                                                                                                                                                                                                                                                                                                                                      PDSTTVIFAGDTNLRDQEVIKCGGLPDNVFDAWEFLGKPKHCQYTWDTKANNNLRIPAAY 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RARGVCSCLALYSPOVVFLQEVIPPYCAYLKKRAASYTIITGNEEGYFTAILLKKGRVKF 201
                                                                                                                                                                                                                                                                                                                                KHRFDRIFFR--AEEGHLIPQSLDLVGLEKLDCGRFPSDHWGLLCTLNVVL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSQETIPFPNTKMMRNLLCVNVSLGGNEFCLMTSHLESTREHSAERIRQLKTVLGKMQEA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSSNYEIITGHEEGXFTAIMLKKSRVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERRPETISEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWNIDGLDLNNLSE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRQPPTSFKSEAYVDLINEDANDTTILEASPS-GTPLEDSSTISFITWNIDGLDGCNLPE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAAEEEGEPEVKKRRLLCVEFASVASCDAAVAQCFLAENDWEMERALNSYFEPPVEESAL 78
                                                                                                                                                                                                                                                                                                                                                                   PESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWDTQMNSNLGITAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                          KSQEIIPFPSTKMMRNLLCVHVNVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQEA
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                                                                  primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                     (first entry)
                                                                                                    sequence SEQ ID NO:13210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,
                                                                  detection;
                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.5%; suc.
68.1%; Pred. No. 2.uc
68.1%; Mismatches
                                                           diagnosis; antisense therapy;
                                                                                                                                                                                                           362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
2.6e-113;
nes 65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as colon cancer
diagnosis of co
                                                           gene therapy
                                                                                                                                                                                                                                                                                                 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a conjunctive comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent buman cDNA sequences; AAB92446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of the comprise of the complementary comprises at least 15 nucleotide comprises at least 15 nucleotides; or (b) a combination of the comprise of the complementary comprises at least 15 nucleotides; or (b) a combination of the comprise of the complementary comprises at least 15 nucleotides; or (b) a combination of the complementary comprises at least 15 nucleotides; or (b) a combination of the complementary complementary comprises at least 15 nucleotides; or (b) a combination of the complementary comprises at least 15 nucleotides or (b) a combination of the complementary complementar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDMAs defined in the specification, and for the detection of diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; SEQ ID 13210;
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                                                    262 PDSTTVIFAGDTNLRDQEVIKCGGLPDNVFDAWEFLGKPKHCQYTWDTKANNNLRIPAAY 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HELI-) HELIX RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                          83 PROPPTSFKSEAYVDLTNEDANDTTILEASPS-GTPLEDSSTISFITWNIDGLDGCNLPE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
PESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWDTQMNSNLGITAAC
                                                                                                                                                   KSQEIIPFPNTKMMRNLLCVNVSLGGNEFCLMTSHLESTREHSAERIRQLKTVLGKMQEA
                                                                                                                                                                                                                                    RARGVCSCLALYSPDVVFLQEVIPPYCAYLKKRAASYTIITGNEEGYFTAILLKKGRVKF
                                                                                                                  KSQEITPFPSTKMMRNLLCVHVNVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQEA
                                                                                                                                                                                                                                                                                                                                                      ERRPETISEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWNIDGLDLNNLSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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2000JP-0183767.
2000JP-0241899.
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99JP-0300253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.5%;
68.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2537pp + CD ROM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1249; DB 22; Pred. No. 3.1e-113;
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English
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Otsuki
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KHRFDRIFFR--AEEGHLIPQSLDLVGLEKLDCGRFPSDHWGLLCTLNVVL

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밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the topoisomerase II binding protein (TopBP) of
the invention. The TopBP protein is useful as an anticancer agent. TopBP
can be used as the target molecule for anticancer agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 12-13; 28pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Topoisomerase II- binding protein - useful as an anticancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHUS ) CHUGAI PHARM CO LTD (TSUR/) TSURUO T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312
                                                        365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 ALSAYFELPENDQGWPRQPPTSFKSEAYVDLTNEDANDTTILEASPS-GTPLEDSSTISF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALNSYFEPPVEESALERRPETISEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLRFDRIFFRAAAEEGHIIPRSLDLLGLEKLDCGRFPSDHWGLLCNLDIIL
NLDIIL 306
                                                        TLNVVL 370
                                                                                                                                                                                                                                                                                                                                                             GYFTAIMLKKSRVKLKSQEIIPFPSTKMMRNLLCVHVNVSGNELCLMTSHLESTRGHAAE
                                                                                                                                                                                                                                                                                                                                                                                         GYFTAILLKKGRVKFKSQEIIPFPNTKMMRNLLCVNVSLGGNEFCLMTSHLESTREHSAE 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITWNIDGLDGCNLPERARGVCSCLALYSPDVVFLQEVIPPYCAYLKKRAASYTIITGNEE 186
                                                                                                                                                  WDTKANNNLRIPAAYKHRFDRIFFR--AEEGHLIPQSLDLVGLEKLDCGRFPSDHWGLLC 364
                                                                                                                                                                                                                                          RMNQLKMVLKKMQEAPESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYT
                                                                                                                                                                                                                                                                   RIRQLKTVLGKMQEAPDSTTVIFAGDTNLRDQEVIKCGGLPDNVFDAWEFLGKPKHCQYI 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITWNIDGLDLNNLSERARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSSNYEIITGHEE 120
                                                                                                                WDTQMNSNLGITAACKLRFDRIFFRAAAEEGHIIPRSLDLLGLEKLDCGRFPSDHWGLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97JP-0251544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97JP-0251544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1154.5; DB 2
Pred. No. 4.2e-104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20; Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362
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Вþ

61

SQEIIPFPSTKMMRNLLCVHVNVSGNELCLMTSHLESTKGHAAERMNQLKMGLKKMQEAP

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RESULT 9
ABG22067
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                                                       Вb
                                                                                      Qγ
                                                                                                                                                                                                                                                          polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The complete recombinate production of (II) and in reaction of chromosome cand gene mapping, and in recombinant production of (II). The complete recombinate production of (II) and in gene therapy techniques for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in clasmostics, forensics, gene mapping, identification of mutations or responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Secrification, but was obtained in electronic format directly from WIPO
                                                                                                                              Best Local Similarity Matches 177; Conserv
                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG22067 standard; Protein; 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAS86254.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #22058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-2002
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              food supplement;
                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences
203 SQEIIPFPNTKMMRNLLCVNVSLGGNEFCLMTSHLESTREHSAERIRQLKTVLGKMQEAP 262
                                                                        143 ARGVCSCLALYSPDVVFLQEVIPPYCAYLKKRAASYTIITGNEEGYFTAILLKKGRVKFK 202
                                                       ARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSSNYEIITGHEEGYFTAIMLKKSRVKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome mapping; gene mapping; gene therapy; forensic; upplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID No 52426; 103pp; English
                                                                                                                                                                                                           263 AA;
                                                                                                                                  Conservative
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                                                                                                                                               48.8%;
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                                                                                                                                  27; Mismatches
                                                                                                                                                   Pred.
                                                                                                                                Score 961; DB 22;
Pred. No. 2.7e-85;
7; Mismatches 23;
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                                                                                                                                                                       Length 263;
                                                                                                                                    Indels
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                                                                                                                                  Gaps
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                                           CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The proper CC polymucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful in gene therapy techniques CC (II). (II) is useful in generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC afood supplement. (II) and its binding partners are useful in medical CL imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC and to produce other types of data and products dependent on DNA and CC and to produce data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO Cast fire wino intent while intents of the invention format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID No 52427; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess bidinostics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000;
23-AUG-2000;
 Sequence
                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                      biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG22068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG22068 standard;
                                                                                                                                                                                                                                                                                                                                                       polypeptide (II) sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-639362/73
)B; AAS86255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSTTVIFAGDINLRDQEVIKCGGLPDNVFDAWEFLGKPKHCQYIWDIKANNNLRIPAAYK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWDTQMNSNLGITAACK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome mapping;
upplement; medical ir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RT,
 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0540217
2000US-0649167
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 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g; gene mapping; gene therapy;
imaging; diagnostic; genetic (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YT;
                                                                                                                                                                                                                                                                                                                                                   (I) is useful as hybridisation probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #22059
                                                                                                                                                                                                                                                                                                                                                                   polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutations
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Query Match

32.9%;

Score 647.5;

DB 22;

Length 311;

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RESULT 11
AAX11868
ID AAX11
AC AAX11
XX AAX11
XX 18-JU
DT 18-JU
DE Human
KW Human
KW Tepro
KW Tepro
XX Homo
XX Homo
XX 11-FE
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AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for human secreted proteins expressed in prostate, and encode the proteins given in AAX11716 to AAX11993 respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene
                                                                                                                                                                                                                     New isolated prostate-derived nucleic acids - used to products which may have cytokine, immune regulatory regulating, anti-inflammatory or tumour inhibition as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                forensic; gene therapy; chromosome mapping; signal peptide; prostate; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopolesis regulation; tissue growth regulation;
                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                         Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
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hes 152; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1999-153780/13.
DB; AAX40590.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAPDSTTVIFAGDTNLRDQEVI-KCGGLPDNVFDAWEFLGKPKHCQYTWDTKANNNLRIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERRPETISEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWEYLMGLDLKQSV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROPPTSFKSEAYVDLTNEDANDTTILEASPS-GTPLEDSSTISFITWN-IDGLD-GCNL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAAEEEGEPEVKKRRLLCVEFASVASCDAAVAQCFLAENDWEMERALNSYFEPPAEESAL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAAQAE-EDRVKRRRLQCLGFALVGGCDPTMVPSVLRENDWQTQKALSAYFELPENDQGW 82
                                                                                                                                                                     34;
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                                                                                                                                                                                                                                                                                                                                                                                                            Dumas Milne
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                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            468
                                                                                                                                                                                                                                            used to develop
latory, haematopoiesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----ERMNQLKMVLKKMQ
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                                                                                                                                                                                                                        activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis;
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RESULT 12
AAG26231
IID AAG26231
AC AAG26
XX ATAbi
XX Prote
KW Prote
KW hybri
KW termi
XX EP10:
XX EP10
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation and differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tunour inhibition activity or other activites. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.
25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

25-MAR-1999

01-APR-1999

01-APR-1999

16-APR-1999

19-APR-1999

21-APR-1999

21-APR-1999

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hybridisation assay; genetic mapping; gene expression control; promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 30610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RARGVCSCLALYSPDVVFLQEVIPPYCAYL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RARGVCSYLALYSPDVIFLQEVIPPYYSYL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERRPETISEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWNIDGLDLNNLSE
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34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                           2000EP-0301439
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99US-0132484.
99US-0132484.
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pred. No. 1.1e-31;
9; Mismatches 45;
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18-JUN-1999;
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99US-0145213.
99US-0145913.
99US-0145918.
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99US-0145918.

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RESULT 13
AAG42551
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Best Local S
Matches 92
25-FEB-1999
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29-OCT-1999
                                                                                                                                                                                 Protein identification; hybridisation assay; ger termination sequence.
                                                                                                         25-FEB-2000;
                                                                                                                           06-SEP-2000
                                                                                                                                               EP1033405-A2.
                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 53080
                                                                                                                                                                                                                                           18-OCT-2000
                                                                                                                                                                                                                                                                                 AAG42551 standard; Protein; 404 AA
                                                                                                                                                               Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                         276
                                                                                                                                                                                                                                                                                                                                                                      LKKR-----AASYTIITGNEEGYFTAILLKKGRVKFKSQEIIPFPNTKMMRNLLCVNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASPSGTPLEDSSTISFITWNIDGLDGCNLPERARGVCSCLALYSPDVVFLQEVIPPYCAY 170
                                                                                                                                                                                                                                                                                                                                           EEGHLIPQSLDLVG---------LEKLDCGRFPSDHWGLLCTLN :: | :::|| :::|| :::|
                                                                                                                                                                                                                                                                                                                                                                                                          VPGRKPLVFATSHLESPCPGPPKWDQMFSRERVEQAKEAIEILR---PNANVIFGGDMNW
                                                                                                                                                                                                                                                                                                                                                                                                                        ASDSGTPLTCLKILSYNVWFREDLE---LNLRWRAIGHLIQLHSPHLICFQEVTPEIYDI 182
                                                                                                                                                                                                                                                                                                                                 DDYKL--GGIEMVGKEAIPGLSYVKEKKVRGDIKKLELPVLPSDHFGLLVTLS 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
92; Conserv
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                                                                                                                                                                                                                                           (first entry)
                                                                                                         2000EP-0301439
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990S-0161405
990S-0161406
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99US-0160981
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99US-0160815
                                                                                                                                                                                          on; signal transduction pathway; metabolic pathway; genetic mapping; gene expression control; promoter;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 275; DB
Pred. No. 5.1e
38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
5.1e-18;
nes 111;
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21-AUG

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     25-FEB-1999;
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                                                                          06-SEP-2000
                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                             termination sequence
                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 30609.
                                                                                                                                                                                                                                                                                                                                                    AAG26230 standard;
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Pred. No. 5.1e-18;
8; Mismatches 111;
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RESULT 15
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                 Protein identification; signal hybridisation assay; genetic termination sequence.
                                                                                         Arabidopsis
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nes 111;
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